

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2005, 20:12:33 ; Search time 19 Seconds
(without alignments)
2643.429 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLVRLKRTWPLEVPETE.....DRFPFRSGRPTDGLRSLFM 522
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues 283416
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.5	8.7	475	2 A86372	53.0K hypothetical
2	187.5	6.8	350	2 H86371	40.0K hypothetical
3	145.5	5.3	547	2 T46366	hypothetical prote
4	128.5	4.7	842	2 T32258	hypothetical prote
5	118	4.3	564	2 H70804	hypothetical prote
6	117.5	4.3	1213	2 A41724	limb deformity (ld
7	117	4.2	403	2 S52796	prp12 protein - hu
8	116.5	4.2	915	2 T12526	hypothetical prote
9	116	4.2	4957	2 T03455	ALR protein - huma
10	116	4.2	5262	2 T03454	ALR protein - huma
11	112	4.1	1006	2 G86292	hypothetical prote
12	111.5	4.0	940	2 JE0291	FB19 protein - hum
13	111	4.0	1097	2 T49187	hypothetical prote
14	110.5	4.0	551	2 S57447	HPBRII-7 protein -
15	110	4.0	424	2 A54964	spliceosome-associ
16	110	4.0	1468	2 S11515	formin - mouse
17	109.5	4.0	742	2 A49672	transcription fact
18	109.5	4.0	772	2 A55004	transcription fact
19	109	4.0	741	2 I48694	probable transcrip
20	109	4.0	1206	2 S24407	formin isoform IV
21	109	4.0	2783	1 A41948	alpha-fetoprotein
22	108	3.9	311	2 T15997	hypothetical prote
23	108	3.9	577	2 T09024	proline-rich prote
24	107.5	3.9	589	2 T29299	hypothetical prote
25	107	3.9	351	1 JSBYPI	centromere-binding
26	107	3.9	505	2 A53152	annexin XI - human
27	107	3.9	1257	2 T01020	hypothetical prote
28	106.5	3.9	212	2 S57330	cathelin-like anti
29	106.5	3.9	584	2 G71676	hypothetical prote

30	106	3.8	401	2 T51407	proline-rich prote
31	106	3.8	444	2 E83802	hypothetical prote
32	105.5	3.8	828	2 T06133	hypothetical prote
33	105.5	3.8	882	2 T43250	spindle pole body-
34	105.5	3.8	897	2 A39405	beta-galactosidase
35	105.5	3.8	1465	2 T23056	chromodomain helic
36	105	3.8	502	2 A55197	Wiskott-Aldrich sy
37	105	3.8	715	2 G86239	protein F20B24.6 [
38	104.5	3.8	235	2 A72594	hypothetical prote
39	104.5	3.8	301	2 JQ1663	hybrid proline-ric
40	104.5	3.8	850	2 JCS047	ras GTPase-activat
41	104	3.8	178	2 T36013	probable integral
42	104	3.8	188	2 D29149	proline-rich prote
43	104	3.8	574	2 H86467	probable transcrip
44	104	3.8	708	2 D96711	hypothetical prote
45	104	3.8	1252	2 D71810	probable type II D

ALIGNMENTS

RESULT 1

A86372
53.0K hypothetical protein F508.33 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86372
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86372
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <STO>
A:Cross-references: UNIPROT:Q9ZUB8; GB:AE005172; NID:G4056460; PIDN:AAC98033.1; GSPDB:GM(C:Genetics:
A:Map position: 1

Query Match 8.7% Score 240.5; DB 2; Length 475;
Best Local Similarity 24.5%; Pred. No. 1.2e-09;
Matches 116; Conservative 89; Mismatches 177; Indels 91; Gaps 20;

QY	1	MRLVRLKRTWPLEVPETEPTLGHRLSHRLSLCTGCGYSSNTFRITITNKDPL--TG 58
DB	3	LRLRHETRETLLKELADAD-TLHDLRRINFTV-----PSSVHLSLNKRDELITPS 53
QY	59	DEETLASVIGSGDILICILQDDIPAPNPSTDSHSLQNNQPSLATSSNOTSQMDE 118
DB	54	PDPTLRLSLIGCDLIYFSLE-----AGESNNWKLKRDSETVASQESNOTSVHD- 102
QY	119	QSDSFQGOAAGSGYWNDDSLGPSQNFPEISIQNAHMAEG--TGFYFSEPM----- 169
DB	103	--SIGF-----AEVDVPPDAKSNPN-----TSVED-----PEGDISGMEPEPMDEQLDM 147
QY	170	--LCSESVEGVPHSLIET--LYQSADCSANDALIVLIHLLMLEGYI--PQOTE----- 218
DB	148	ELAAAGSKELSPFFFLKNILLESKSGDTSLT-TLALSVHVMLESFVLLNHGSKDNFS 206
QY	219	AKALSNPEKWKLSGVYKLYQYHPLCEGSSATITCVPLGNLIVVNATL-----KINNEI-- 271
DB	207	KELLATVSLRYTLPELIKSKDNTI---ESVSKVQNLGPVWVYGVTVGSSGRVHVNLDK 263
QY	272	-RSVKRLQLPSPFCICEKLGENVANIYKDLKSLFKDLQVYPLLATRQALNLPDVF 330
DB	264	RRFVPIVDLVMOTSTSDSDE---EGSSSIYREVFMFWMVKDRVLVPLLIIGICDKAGLEPPP 320

QY 331 GLVPLPLELKLRIFRLLDVRSLVSACVCDLFTASNDPLLRFLYLRFRDNTVRV--Q 388
Db 321 CLMRPLTELKLELLELPGVSGNMACVCTEMRYLASDNDLWKQKCLEVNVFVTEAGD 380
QY 389 DTDWK-----ELVRKHRIQKESPKGRFVMLLPSTHTIPF 424
Db 381 SVNWKARFATFWKQGLAAASDTFWRQNLGRNISTGRSGIRFPRIIGDPPF 433

RESULT 2

40.0K hypothetical protein F508.32 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86371
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Razzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86371
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <STO>
A:Cross-references: UNIPROT:Q9ZUB9; GB:AE005172; NID:g4056459; PIDN:AAC98032.1; GSPDB:GN
C:Genetics:
A:Map position: 1

Query Match 6.8%; Score 187.5; DB 2; Length 350;
Best Local Similarity 24.4%; Pred. No. 5.2e-06;
Matches 90; Conservative 58; Mismatches 118; Indels 103; Gaps 17;
QY 172 SESVEGQVPHSLF-----TLQSADCSNDANDALIVLIHLLMLESGLV 213
Db 22 NSGIEGVPMDVELAAAKSKRLSEPFLLKNVLEKSGDTSDLT-ALALSVAHVLMESGFV 80
QY 214 --PQOTE-----AKALSPEKWKLSGVYKLYQMHPCLCESSATLTCVPLGNLIVNATL- 265
Db 81 LUDHSDKFSFKLLSVSLRYTLPELITRKDNTV---ESVTVRFQNIQGLVVGTLG 137
QY 266 ----KINNEIRSVKRLQLLPESFICEKL---GENVANIYKDLQKLSRLFKDLQVYPLLA 318
Db 138 GSKCRVH--MTSLDKSRFLPVDLVDTLKFEKQSGSSYREVFVLMWRMVKDELVIPLL- 194
QY 319 FTRQALNLPDVFQ-----LVVLPLELKLRIFRLLDVRSLVSACVCDLFTASNDPLLV 372
Db 195 -----IGLCKAGLESPPCLMLLPTLELKLLELPGVSGNMACVCTEMRYLASDNDLW 249
QY 373 RPLYLRDRFRDNTVRVQ--DTWKELY-----RKR--HQRKESPKGRFVMLLPSTHTIP 423
Db 250 EHKCLEEGKGLWLYTGDVDMKRFASFWRKRLLDLARRNPPIKK----- 296
QY 424 FVFNPLHRPPSPSRLLPGIIGGEYDQRTPLPYVGDPISSILIPGGETPSQPPL----- 478
Db 297 --SNRFPFTLPDRR-----DRREPPDRFG-----PSDFYRFRGLRDP 331
QY 479 RRFDPVGP 487
Db 332 RDRFGPRDP 340

RESULT 3

T46366
hypothetical protein DKFZp434C0118.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46366
R:Ottensmeyer, B.; Obermaier, B.; Mewes, H.W.; Cassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23031
A:Accession: T46366
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-547 <AAA>
A:Cross-references: UNIPROT:Q9NT57; EMBL:AL1137520
A:Experimental source: adult testis; clone DKFZp434C0118
C:Genetics:
A:Note: DKFZp434C0118.1

Query Match 5.3%; Score 145.5; DB 2; Length 547;
Best Local Similarity 21.7%; Pred. No. 0.011;
Matches 98; Conservative 61; Mismatches 123; Indels 169; Gaps 24;
QY 105 SLATSSNTSQMDQPSDFQQAQSGVWVNDMSMLG-PSQNFEAESIQDNAHMAEGTGF 163
Db 72 SAAETGRSRHPTDQHPSS--GGRCRGGTESPSAAGRASPMAEAE--EDCH----- 119
QY 164 YPSEPMLCSESVGGVPHSLLETLYQSADCSNDANDALIVLIHLLMLESYIPGCTEAKA-L 222
Db 120 -----SDTVR-----ADDBENES-----PAETDLQAOL 143
QY 223 SMPEKWKLSGVYKLYQMHPCLCEG--SSATLTCVPL---GNLIVVNAVTLKINNE----- 270
Db 144 QM-----FRAQMPFELAPGVSSNLENRPCRAAGSLQKTSADTKGKEQAEKKA 194
QY 271 ----IRSV-----KRLQLPE-----SFICKEKLGENVANIY---KDLQ 302
Db 195 RELFLKAVEEQNGALYEAIRFYRRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDS 254
QY 303 KLSRL---FKDLVYPLLAFTQALNL--PDV-----FGLVLPLELKLRIFRLL---LD 348
Db 255 KNADLLSYFQQQ-----LTFQESVLKLCQPELESQIHSVLPMELVMYIFRWVSSDL 309
QY 349 VRSVLSLSAVCRDLFTASNDPLLRFLYLRFRDNTVRV--VQDMDKELYRKRHIQRKES 407
Db 310 LRSLEQLSLVRCGFICARDPEIWRKLCKVGRSCIKLVPTYSWREMFLE-----P 362
QY 408 KGRFVMLLPST-----HTIPFYNPLHRPPSPSRLLPGIIGGEYDQ 450
Db 363 RVRFPGVYISKTYTIRQGESLDGFYRAWHQVEYI---RYIRFFPDGHV----- 408
QY 451 RPTLPYVGDPISSILIPGGETPSQPPLRPR 481
Db 409 -----MMLTTPPEPQSIYVRLRTR 427

RESULT 4

T32258
hypothetical protein C24A1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32258
R:Connell, M.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid C24A1.
A:Reference number: Z21141
A:Accession: T32258
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-842 <CON>
A:Cross-references: UNIPROT:O17055; EMBL:AF024491; PIDN:AAB70312.1; GSPDB:GN000021; CESP:
A:Experimental source: strain Bristol N2; clone C24A1
C:Genetics:
A:Gene: CESP:C24A1.3
A:Map position: 3
A:Introns: 43/2, 189/3; 234/1; 351/1; 511/3; 578/3; 594/2; 636/2; 675/3
Query Match 4.7%; Score 128.5; DB 2; Length 842;
Best Local Similarity 20.3%; Pred. No. 0.35;

[illegible]

QY	467	-----GPGETPSQF-----PPLURPRF-----DPVGPPLPGNPILPGRCGPNDRFPFRPSRGR	513
Db	685	PPLTGPTSVTPHFAFGPPLLPQLSEGCRDFQAPAPAPPLPGLGPPVP-PPLPGSSGL	742

Qy 514 P 514
Db 743 P 743

```

RESULT 7
S52796
    prpl2 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 10-Nov-1995 #text_change 10-Sep-1997
C:Accession: S52796
R:Ruhlmann, A.; Kreideweiss, S.; Nordheim, A.
  submitted to the EMBL Data Library, March 1995
A:Reference number: S52796
A:Accession: S52796
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-403 <RUH>
A:Cross-references: EMBL:X86019; NID:g762950; PID:g762351

```

Query Match	4.2%;	Score 117;	DB 2;	Length 403;
Best Local Similarity	32.9%;	Prod. No. 0.8;		
Matches	46;	Conservative	9; Mismatches 41;	Indels 44; Gaps 9
Qy	415	LPSSHTTTFYPNPUHPPFPSSR----	LPGLIGGEYDQRPTLPVVGDPISSL--	IP 466
Db	203	VPSTPR--PSAPHRHLPPPPSRGCPPLPSSGN--	DEIPLPQRMLSUSSSTPPLP	258
Qy	467	GPGET-----PSOFFPLRPRFDP--	VGCLPGPNPI-----	LPG----- 497
Db	259	SPGRSGPLPPVPSERPVPPVDRDPGRSGPLPPPPVSRNGSTSRALPATPQLPSPRSGVD		318
Qy	498	--RGGNDRF--PFRPSRGRP	514	
Db	319	SPRSGPRPLPPDRPSAGAP	338	

```

RESULT 8
T12526
hypothetical protein DKFZp434M183.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12526
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17524
A:Accession: T12526
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-915 <WAM>
A:Cross-references: UNIPROT:Q9Y4Q8; EMBL:AL080141
A:Experimental source: adult testis; clone DKFZp434M183
C:Genetics:
A:Note: DKFZp434M183.1

```

Query Match	4.2%	Score 116.5	DB 2	Length 915
Best Local Similarity	20.7%	Pred. No. 2.9		
Matches 129	Conservative 76	Mismatches 208	Indels 209	Gaps 36
Qy	34	LLCTWGYSSNTRFTITLNY-KDPLTGDEETLASYGIVSGDLLCLILQDDIPAPNTPSSDT	92	
Db	205	LKVLTLEQDSRMKFLKLLGYSKDEL---OKKVATW-----LKSDV---GLGESQP	247	
Qy	93	SEHSSLQNEOPSLSATSNQTSMDQEQSDSFQGOAAQSGV-W-----NDDSM-----	139	
Db	248	PKGNDLNSDROAFQCSQAKHTTKEASAPFDELVPQNMTWPIPTKIDGLLSQAL	307	
Qy	140	----LGPSON---FEAESIQDNAHMAEGTGF-----YPSEPMLCSVEGVGPHSLTLYOS	189	

Db 308 LLGELGPVAVELCLBEERFADAILLAQAAGTDLLLKQTERYLAKKKT--KISSLLACVVQK 365
 Qy 190 -----ADCS DAN--DALIVLHLLMESGYIPQGTAKALSMPEKWKSLGVYKLOYMHP 241
 Db 366 NWKDVVCTCSLKNWREALALLTY-----SGTE-----KPPELCDMLGTRMEQ---- 408
 Qy 242 LCEGSSATLTCVPLGNLIVWNATLKINNEIRSVKRLQLLPESFICK---EKLGENVANIY 298
 Db 409 --EGSRA-----LTSEARL-----CYVCSGSVERLVECMACKH 439
 Qy 299 KDLOKLSRLFXDQLVYPPLAFTRQALNLPDVFGLVVLPLELKLRIFRLLDVRSVL----- 353
 Db 440 ---QALSPMALQDLMKVMVNLRSLEQLRGPHGVSPG---ATTYRVTOYANLLAAQGS 492
 Qy 354 ---SLSAVCRD-----LFTASNDPLLMR-----FLYLDRDPRDNTVRVQDTDWKE 394
 Db 493 LATAMSFPLRCAQPPVQOQLRDLFHAQSAVLGQOQSPFPFPRIVVGVTLHSETTSYR 552
 Qy 395 L-YRKHRIQRKESPKGRFVMLLPSSHTHTIPFYENPLHPRPPPSR----- 438
 Db 553 LGSQFSHVQVTPSPRPR--VFTPQSPAMPLAPS--HPSFYQGPRQNIISDYRAGPQAI 608
 Qy 439 ---LPPGI-----IGGEYDQRP-----TLPYVGDPISSLI PG---PG-----E 470
 Db 609 QPLPLSPGVRPASSQPQLLGQGVQVQVNPVPGFPGTWPLPGSPLPMPACPGIMRPGSTSLPE 668
 Qy 471 TPSQFP--PLRP-----RFPDVGPLPGPNILPG-----RGSPND 503
 Db 669 TPLRFLPLPLRPLGPRMVSHTPAPPASFPVPLPGDPCGAPCSSVLPTTGTILTPHPGPQD 728
 Qy 504 RFPFRPS-RGRPTDGR L--SFM 522
 Db 729 SWKEAPAPRGNLQRNKLPETFM 750

RESULT 9
 T03455
 ALR protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T03455
 R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, Oncogene 15, 549-560, 1997
 A:Title: Structure and expression pattern of human ALR, a novel gene with strong homology
 A:Reference number: Z14954; PMID:97388474; PMID:9247308

RESULT 9
T03455
ALR protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03455
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, C.
Oncogene 15, 549-560, 1997
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homology
A:Reference number: Z14954; MUID:97388474; PMID:9247308
A:Accession: T03455
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-4957 <PRA>
A:Cross-references: UNIPROT:O14586; EMBL:AF010404; NID:G2358286; PIDN:AAC51735.1; PID:G2358286
C:Genetics:
A:Gene: ALR
A:Map position: 12
C:Superfamily: acute lymphoblastic leukemia protein, ALR type
C:Keywords: alternative splicing

	Query Match	4.2%	Score 116;	DB 2;	Length 4957;
	Best Local Similarity	20.0%;	Pred. No. 3;		
	Matches 102; Conservative	64;	Mismatches 181;	Indels 164;	Gaps 25;
Qy	94 EHSSIQNNEOPSLATSSNOTSMODEQPDSFGOAAQS--GWND-D-SMLGPSONFEAES	150	:	:	:
Dd	3356 QQQQLQQQQQQQQQLQQQQQQQQQQQQQQQQQQQQMGLLNQSRLLSPQQ-	3409	:	:	:
Qy	151 IQDNAHMAEGTGFPSEPM-----LCSESVE-----	176	:	:	:
Dd	3410 -QQQQQVALGPGM-PAKPLQHFPSSPCALGPTLLLLTCGEQTVDPAVSSEATEGPSITHGG	3467	:	:	:
Qy	177 ----GOVPHSILETYQSADCSDDANDALIVLIHLMLLESYIPO-GTEAKALSMPKEKWLS	231	:	:	:
Dd	3468 PLAIGTTPESMATEGEVKPSSLGSQSLILVV-----POPQPPSSLOLQPPURLP	3518	:	:	:

```
QY 232 GYKIQ--YMH-----PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP 281
Db 3519 GQQQQVSLHTTAGGSHGQLGSGSSSEASSVP---HLLAQPSVSLGDPQGSMTQNLILGP 3575
QY 282 ESFICKEKLGENVANYKDLQKLSLFDQLVYVPLLAFTROALNLPDVFGLVVLPLEKL 341
Db 3576 QQPMLEPMQNTGP-----QPPKPGVL---QSQGLP---GVCIMTVGQL 3617
QY 342 RIFRLDVRSLVLSAVCRDLFTASNDPLLWFLYLRDRFRONTVRVQDTWKELYRKHI 401
Db 3618 R-----AQLGVLAKNPQLRHLSPQQOQL-----QALLMQRL 3651
QY 402 QKESPKGRFVMLLP-----SSTHTIPF-----YNNP-----LHPRPFP 436
Db 3652 QQSQA-----VRQTPPYQEPGTQTSPLQGLLCCQQLGFGPGFTGQLQELGAGRPQGP 3706
QY 437 SRL--PPGIIGGEYDQRTPLPVG-----DPISSLIPGGETPSPFPPLRPFRDVGPLP 489
Db 3707 PRLPAPPGALS-----TGPVLGPHVHTPPSS--POEPKRPSPQLPSPSSQLPTEAQLP 3757
QY 490 GNPILPGRGGPNDRFPPRPSGRPTDGRLS 520
Db 3758 PTHGTPKPGQPTLEPP--PGRVSPAAAQLA 3786

RESULT 10
T03454
ALR protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03454
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano,
Oncogene 15, 549-560, 1997
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homology
A:Reference number: Z14954; MUID:97388474; PMID:9247308
A:Accession: T03454
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5262 <PRA>
A:Cross-references: UNIPROT:O14686; EMBL:AF010403; NID:g2358284; PIDN:AACS1734.1; PID:g2
C:Superfamily: acute lymphoblastic leukemia protein, ALR type
C:Keywords: alternative splicing

Query Match 4.2%; Score 116; DB 2; Length 5262;
Best Local Similarity 20.0%; Pred. No. 41;
Matches 102; Conservative 64; Mismatches 181; Indels 164; Gaps 25;

QY 94 BHSLLQNNNEQPSLATSSNQTSMDQPSDSFOGQAQS--GVWDD-SMLGPSQNFSAES 150
Db 3661 QQQQLQQQQQLQQQQQLQQQQQLQQQQQLQQQQQLQQQQQLQQQQQLQQQQQLQQQQQL 3714
QY 151 IQDNHMAEGTFYPSSEPM-----LCSESVE----- 176
Db 3715 -QQQQQVALPGM-PAKPLQHFSSPCALGPTLLLTGKEQNTVDPASVEATEGSPTHOQG 3772
QY 177 ---GQVSHLETLQSDACSDANALIVLHLLMESGYIPO-GTEAKALSMPEKWLK 231
Db 3773 PLAIGTTPESMATREGEVKVPSLGSQQLLVQ-----PQOPQSSQLQPLPLP 3823
QY 232 GYKIQ--YMH-----PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP 281
Db 3824 GQQQQVSLHTTAGGSHGQLGSGSSSEASSVP---HLLAQPSVSLGDPQGSMTQNLILGP 3880
QY 282 ESFICKEKLGENVANYKDLQKLSLFDQLVYVPLLAFTROALNLPDVFGLVVLPLEKL 341
Db 3881 QQPMLEPMQNTGP-----QPPKPGVL---QSQGLP---GVCIMTVGQL 3922
QY 342 RIFRLDVRSLVLSAVCRDLFTASNDPLLWFLYLRDRFRONTVRVQDTWKELYRKHI 401
Db 3923 R-----AQLGVLAKNPQLRHLSPQQOQL-----QALLMQRL 3956
```

```
QY 402 QKESPKGRFVMLLP-----SSTHTIPF-----YNNP-----LHPRPFP 436
Db 3957 QQSQA-----VRQTPPYQEPGTQTSPLQGLLCCQQLGFGPGFTGQLQELGAGRPQGP 4011
QY 437 SRL--PPGIIGGEYDQRTPLPVG-----DPISSLIPGGETPSPFPPLRPFRDVGPLP 489
Db 4012 PRLPAPPGALS-----TGPVLGPHVHTPPSS--POEPKRPSPQLPSPSSQLPTEAQLP 4062
QY 490 GNPILPGRGGPNDRFPPRPSGRPTDGRLS 520
Db 4063 PTHGTPKPGQPTLEPP--PGRVSPAAAQLA 4091

RESULT 11
G86292
Hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86292
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroo, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G86292
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1006 <STO>
A:Cross-references: UNIPROT:O9LMQ1; GB:AE005172; NID:g8927662; PIDN:AAF82153.1; GSPDB:GN
C:Genetics:
A:Map position: 1

Query Match 4.1%; Score 112; DB 2; Length 1006;
Best Local Similarity 32.7%; Pred. No. 7;
Matches 36; Conservative 6; Mismatches 48; Indels 20; Gaps 3;

QY 406 SPKGRFVMLPSTHTIPFYNPLHPRFPSPRLPPLPGIIGGEYDQRTPLPVYGDPISSL 465
Db 88 SPENPFLFPQ-----PRPPRRPRPRPRSPRLFP-----PLVSPSPPLH 128
QY 466 PPGGETPSPFPPLRPFRDVGPLGPNILPGRGPN-DRPFRPSPRGP 514
Db 129 PRPSPCPPLPSPPLVSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 178

RESULT 12
J50291
FB19 protein - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: J50291
R:Totaro, A.; Grifa, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roetto, A.; Zelante
Biochem. Biophys. Res. Commun. 250, 555-557, 1998
A:Title: Cloning of a new gene (FB19) within HLA class I region.
A:Reference number: J50291; MUID:99003493; PMID:9784381
A:Accession: J50291
A:Molecule type: mRNA
A:Residues: 1-940 <TOT>
A:Cross-references: UNIPROT:O00405; GB:Y13247; NID:g2117158; PIDN:CAA73697.1; PID:g21171
C:Genetics:
A:Gene: FB19
A:Map position: 6p21.3

Query Match 4.0%; Score 111.5; DB 2; Length 940;
Best Local Similarity 36.8%; Pred. No. 6.9;
Matches 39; Conservative 6; Mismatches 40; Indels 21; Gaps 6;
```

QY 424 FYPNPLHPRPPSSRLPPGIIGGYDQRTPLPYVGDPISSLIIPGGETPSQFPPLRPRFD 483
Db 643 FPPGGGMPGPHGG-PGGVGPRLGGPPPPRGGDPWD---GPGD-PMRGGPNRG--- 694
QY 484 PVGULPGNPLPGRGG-----PNDRPFPFRSR-----GRPTDGR 518
Db 695 --GPGGPGVYHRGGRGGNEPPPPPPPPFRGARGRGSGGPPNCR 738

RESULT 13

T49187
Hypothetical protein MAA21.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49187
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Meves, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25018
A:Accession: T49187
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1097 <RIE>
A:Cross-references: UNIPROT:Q9LY69; EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.90
A:Experimental source: cultivar Columbia; BAC clone MAA21
C:Genetics:
A:Gene: ATSP:MAA21.90
A:Map position: 3
A:Introns: 106/2; 124/3; 165/3; 198/1; 210/2; 245/3; 265/1; 297/3; 337/3; 352/1; 394/1;

Query Match 4.0%; Score 111; DB 2; Length 1097;
Best Local Similarity 20.2%; Pred. No. 9.4;
Matches 111; Conservative 75; Mismatches 218; Indels 146; Gaps 26;
QY 37 TWGY-----SNTFTTLNKKDLTDEETLASYGVSGDLICLIQDD-IPAPN 86
Db 435 TWGLLKIMFEEBGTSTRLKLSHLGFTLVAEKDQAVDG---LSSDLNGIRLEDTAADALD 491
QY 87 IPSSTDSHSSLOANEQ-----PSLATSSNOTSMODEOPSD---SFOGAAQSGVWNDD 138
Db 492 LDDSEAAAFAMNGEDFNFPAPKPDTPVTSKADFMPSDTPSTKGEETQEMOESEE 551
QY 139 MLGP-----SQNFEAESIQDN---AHMAEGTGFTYPS---EPMCLSES 174
Db 552 SSDPVFDNAIQRALIVGDYKEAVDQCITANKWADALVIAHVG-GTALWESTREKYLKTS 610
QY 175 -----VGGQPHSLLETLYQSADCDANDALIVLHLLMLESYIPQGTAKALSMPEKW 228
Db 611 APYMKVSAWVNDLRSILYTRSHKFWKETLALLC-----TFAQGEQW 653
QY 229 KLSGVYKLYMHPLCEGSSATITCVPLGN-LIVVNATLKINNEIRSVKRLQLLPESFICK 287
Db 654 T-----TLCDALASKL--WAAGNTLAALVCYCAGNVDRIVE-----INRSLSAN 696
QY 288 EKLGENVANIYKDLQKLSRLFKDQIVYPLLA----FTRQALMLPDVFGVLVLP----LELK 340
Db 697 ERDGRSYAELLQDLMKLT-----LVLATGNKKFSASLCKLPESYAEILLASQGLTTA 750
QY 341 LAIFRLLD-----VRSVLSLSAVCRDLFTAS-----NDPLLRFVLYR 378
Db 751 MKYLVLDSSGGLSPELSILDRISLSABFETNTTASGNTPOQSTPMYQNQETQAQPNVLA 810
QY 379 DFRDNTVRVQDQDMKELYRKRIQRKESPKGRFVMLLPSSSTHTIP---FYFNPLHPRFP 435
Db 811 NPYDNOYQOPTYDSYVVFQVSH-----FPMQPTWFMFHQAQPAQPSFTAPT--SNAQP 864
QY 436 SSR-----LPPGIIGGYDQRTPLPYVGDPISSLIIPGGETPSQFPPLRPRFDVGPL- 488
Db 865 SMRTTFVSTPALKNADQYQOPTMS-----SHSFTGTGSNNAYVPVPPGQYAFSGFSQ 918
QY 489 --PGNPNILP 496
Db 919 LQYENPKMP 928

RESULT 14

S57447
HPRII-7 protein - human
N:Alternate names: HPRII-4 protein
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S57447; S57489
R:Fleischhauer, K.L.
submitted to the EMBL Data Library, June 1992
A:Reference number: S57447
A:Accession: S57447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <FILE>
A:Cross-references: UNIPROT:Q16630; EMBL:X67336; NID:9871300; PIDN:CAA47751.1; PID:987133
A:Experimental source: ribonucleoprotein repeat homology
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-551 <FL2>
A:Cross-references: EMBL:X67337; NID:9871298; PIDN:CAA47752.1; PID:9871299
C:Genetics:
A:Introns: 231/3
A:Superfamily: ribonucleoprotein repeat homology
F:82-151/Domain: ribonucleoprotein repeat homology <RRM4>

Query Match 4.0%; Score 110.5; DB 2; Length 551;
Best Local Similarity 31.1%; Pred. No. 3.7;
Matches 41; Conservative 9; Mismatches 39; Indels 43; Gaps 8;
QY 408 KGRFVMLLPSTHTTPFYVNPPL-----HPRPPSSRLPPGIIGGYDQRTPLPYVGDPISS 463
Db 204 RGRPGAVGGDR-----FPGAGPGGPPPPAGGTPP-----RPLGPPGPPGPP 250
QY 464 LIPGGET---PSQFPPLR-----PRFDVGPL-PGNPILPGRGGPN 502
Db 251 GPPPPGQVLPPLAGPPNRRDPPPPVLPFGQPPFQP---PLGLPPGPPPPVPGYGGPP 307
QY 503 DRFPFRPSRGRP 514
Db 308 G-PPPPQQGPP 317

RESULT 15

A54964
spliceosome-associated protein SAP-49 - human
C:Species: Homo sapiens (man)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: A54964
R:Champion-Arnaud, P.; Reed, R.
Genes Dev. 8, 1974-1983, 1994
A:Title: The prespliceosome components SAP 49 and SAP 145 interact in a complex implicat
A:Reference number: A54964; MUID:95047348; PMID:7958871
A:Accession: A54964
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-424 <CHA>
A:Cross-references: UNIPROT:Q15427; GB:L35013; NID:g556216; PIDN:AAAG0300.1; PID:g556217
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein
F:14-81/Domain: ribonucleoprotein repeat homology <RRM4>
F:101-169/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 4.0%; Score 110; DB 2; Length 424;
Best Local Similarity 32.0%; Pred. No. 2.8;
Matches 39; Conservative 9; Mismatches 32; Indels 42; Gaps 9;
QY 430 HRPFPSSRLP-PGI-----IG-----GEYDQRTPLPYVGDPISSLIIPGPG 469
Db 292 HPHPFPFGMPHFGMSQMLAHGHGHPAGPPGSGGQPPPPPPPG-----MPHPG 345
QY 470 ETPSQFPPLRPRF-DFV---GFLP-----GNPILPGRG--GPNDRFFRPSRG-----R 513

Db 346 PPFMCMPPRGPFEGSPMGHGPMPPHCMRGPPPLMPPHCGYTGPPRPPPYGYORGLPPPR 405

Qy 514 PT 515

||

Db 406 PT 407

Search completed: July 19, 2005, 20:20:14
Job time : 22 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2005, 20:09:48 ; Search time 171 Seconds
(without alignments)
1563.189 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 2754

Sequence: 1 MRLRVLLKRTWPLEVPETE.....DRFPFRPSGRPTDRLSLFM 522

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2748	99.8	522	1	FBX7_HUMAN	Q9Y211 homo sapien
2	1984	72.0	522	2	Q6RFS3	Q6RFS3 rattus norv
3	1977.5	71.8	523	2	Q8K0A5	Q8K0A5 mus musculus
4	1295	47.0	361	2	Q6Y0L7	Q6Y0L7 gallus gall
5	1125	40.8	478	2	Q6DE59	Q6DE59 xenopus lae
6	240.5	8.7	475	2	Q9ZUB8	Q9ZUB8 arabidopsis
7	205	7.4	776	2	Q8GZV6	Q8GZV6 oryza sativ
8	187.5	6.8	350	2	Q9ZUB9	Q9ZUB9 arabidopsis
9	147	5.3	270	1	PSF1_DROME	Q9V637 drosophila
10	145.5	5.3	434	2	Q9V593	Q9V593 homo sapien
11	144	5.2	403	2	Q6PKH7	Q6PKH7 homo sapien
12	144	5.2	437	2	Q9NT57	Q9NT57 homo sapien
13	144	5.2	447	1	FBX9_HUMAN	Q9UK97 homo sapien
14	138.5	5.0	356	2	Q7ZTY2	Q7ZTY2 brachydanio
15	135	4.9	436	2	Q8VDY6	Q8VDY6 mus musculus
16	135	4.9	437	2	Q8BK06	Q8BK06 mus musculus
17	134.5	4.9	1183	2	Q7TSH6	Q7TSH6 mus musculus
18	134.5	4.9	1209	2	Q6PFF0	Q6PFF0 mus musculus
19	134	4.9	3148	2	Q8B6Q8	Q8B6Q8 poncirus tr
20	129.5	4.7	1200	2	Q69ZP8	Q69ZP8 mus musculus
21	129	4.7	745	2	Q6Z1Z5	Q6Z1Z5 oryza sativ
22	128.5	4.7	850	2	Q17055	Q17055 caenorhabdi
23	126.5	4.6	431	2	Q7SV92	Q7SV92 xenopus lae
24	126	4.6	355	1	FX32_HUMAN	Q969P5 homo sapien
25	123	4.5	271	1	PSF1_HUMAN	Q92530 homo sapien
26	123	4.5	936	2	Q8QRV7	Q8QRV7 pongine her
27	122	4.4	953	2	Q6MB50	Q6MB50 parachlamyd
28	120.5	4.4	888	2	Q6P9Q5	Q6P9Q5 mus musculus
29	120.5	4.4	911	2	Q8CIE2	Q8CIE2 mus musculus
30	120.5	4.4	925	2	Q8NFF4	Q8NFF4 homo sapien
31	120	4.4	271	2	Q8BHL8	Q8BHL8 m mus muscu

RESULT 1

ID	FBX7_HUMAN	STANDARD;	PRT;	522 AA.
AC	Q9Y311; Q96HM6; Q9UF21; Q9UKT2;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	F-box only protein 7.			
GN	Name=FBX07; Synonym=FBX7;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE OF 41-522 FROM N.A.			
RX	MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;			
RA	Cenciarelli C., Chiar D.S., Guardavaccaro D., Parks W., Vidal M.,			
RA	Pagano M.;			
RT	"Identification of a family of human F-box proteins."			
RL	Curr. Biol. 9:1177-1179(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20059565; PubMed=10945468; DOI=10.1006/geno.2000.6211;			
RA	Ilyin G.P., Riand M., Pigeon C., Gugen-Guilouzo C.;			
RT	"cDNA cloning and expression analysis of new members of the mammalian			
RL	F-box protein family."			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;			
RA	Dunham I., Hunt L.R., Collins J.E., Bruskewich R., Beare D.M.,			
RA	Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,			
RA	Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,			
RA	Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,			
RA	Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,			
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,			
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,			
RA	Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,			
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,			
RA	Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,			
RA	Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,			
RA	Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,			
RA	Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,			
RA	Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,			
RA	McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,			
RA	Odeh C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,			
RA	Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,			
RA	Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,			
RA	Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,			
RA	Vaudin M., Wallis J.M., Whiteley M.N., Willey D.L.,			
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,			
RA	Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,			
RA	Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,			
RA	Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,			

ALIGNMENTS

32	120	4.4	684	1	CDC4_CANAL	P53699 candida alb
33	120	4.4	1255	2	Q9R2J6	Q9R2J6 plaamid col
34	119	4.3	271	2	Q8C0G9	Q8C0G9 mus musculu
35	119	4.3	287	2	Q95UG5	Q95UG5 babesia bov
36	119	4.3	844	2	Q9R2J5	Q9R2J5 plaamid col
37	118	4.3	442	2	Q9VG61	Q9VG61 drosophila
38	118	4.3	564	2	O53539	O53539 mycobacteri
39	118	4.3	564	2	Q7TWD7	Q7TWD7 mycobacteri
40	117.5	4.3	503	1	WAIP_HUMAN	O43516 homo sapien
41	117.5	4.3	1179	2	Q9NQW1	Q9NQW1 homo sapien
42	117.5	4.3	1213	1	FMN_CHICK	Q05858 gallus gall
43	117	4.2	2167	1	SHK1_RAT	Q9W48 rattus norv
44	116.5	4.2	210	2	Q8TC93	Q8TC93 homo sapien
45	116.5	4.2	592	1	ODP2_DICDI	P36413 d dihydroll

RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.I.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wansley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Haller L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RA Nature 402:489-495(1999).
RL [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -!- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
CC (By similarity).
CC -!- SIMILARITY: Contains 1 F-box domain.
CC -----
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CC EMBL; AF232225; AAF67155.1; -;
CC EMBL; AL050254; CAB43356.1; -;
CC EMBL; Z71183; CAB63143.1; -;
CC EMBL; BC008361; AAH08361.1; -;
CC Genew; HGNC:13586; PBX07.
CC MIM; 605648; -;
CC GO; GO:0000151; Cubiquitin ligase complex; TAS.
CC GO; GO:0004842; Fubiquitin-protein ligase activity; TAS.
CC GO; GO:0006511; Fubiquitin-dependent protein catabolism; TAS.
CC InterPro; IPR001810; F-box.
CC InterPro; IPR008945; Skp1_Skp2.
CC Pfam; PF00646; F-box; 1.
CC PROSITE; PSS0181; FBOX; 1.
KW Ub1 conjugation pathway.
DOMAIN 329 375 F-box.

FT CONFLICT 41 41 S -> M (in Ref. 1).
FT CONFLICT 79 79 Q -> H (in Ref. 1).
FT CONFLICT 84 84 A -> P (in Ref. 1).
FT CONFLICT 115 115 M -> I (in Ref. 1 and 4).
FT CONFLICT 169 169 M -> L (in Ref. 1).
FT CONFLICT 224 224 M -> L (in Ref. 1).
FT CONFLICT 241 241 P -> H (in Ref. 1).
FT CONFLICT 328 328 D -> N (in Ref. 1).
FT CONFLICT 413 413 M -> L (in Ref. 1).
FT CONFLICT 475 475 F -> L (in Ref. 1).
SQ SEQUENCE 522 AA; 58502 MW; C4E5E70A0747287A CRC64;
Query Match 99.8%; Score 2748; DB 1; Length 522;
Best Local Similarity 99.8%; Pred No. 3 9e-174;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRLRVRLKRTWPLEVPEPETLGLHRLSHRLSLCTWGYSSNTFTITLNYKDLTGDE 60
DB 1 MRLRVRLKRTWPLEVPEPETLGLHRLSHRLSLCTWGYSSNTFTITLNYKDLTGDE 60
QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLOHNEOPSLATSSNOTSMDROP 120
DB 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLOHNEOPSLATSSNOTSMDROP 120
QY 121 SDSFGQAAQSGVWDDSMGLGFSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
DB 121 SDSFGQAAQSGVWDDSMGLGFSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
QY 181 HSLETLYSADCSANDALIIVLIHLLMESGYIPQGTAKALSMPEKWLKSLGVYKLYQVNH 240
DB 181 HSLETLYSADCSANDALIIVLIHLLMESGYIPQGTAKALSMPEKWLKSLGVYKLYQVNH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATKINNEIRSVKRLLOLLPESFICKEKLGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVVNATKINNEIRSVKRLLOLLPESFICKEKLGENVANIYKD 300
QY 301 LQKLSRLFKDQVLPVLLAFTQAALMLPDVGLVLPVLEKLRIFRLDLVRSVLSAVCR 360
DB 301 LQKLSRLFKDQVLPVLLAFTQAALMLPDVGLVLPVLEKLRIFRLDLVRSVLSAVCR 360
QY 361 DLFTASNDPLWRFLYLDRDNDTVRVQDTWKELYRKRHQKESPKGRFVMLLPSSSTH 420
DB 361 DLFTASNDPLWRFLYLDRDNDTVRVQDTWKELYRKRHQKESPKGRFVMLLPSSSTH 420
QY 421 TIPFPVNPVLPHPSPSSRLPGIIGGEYDQRPVGDPTLVGDSLLIPGCGTSPQPPPLRP 480
DB 421 TIPFPVNPVLPHPSPSSRLPGIIGGEYDQRPVGDPTLVGDSLLIPGCGTSPQPPPLRP 480
QY 481 RFDVPVGPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPV 522
DB 481 RFDVPVGPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPV 522
RESULT 2
Q68FS3 PRELIMINARY; PRT; 522 AA.
AC Q68FS3;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RC SEQUENCE FROM N.A.
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Moore T., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Moore T., Wang J., Hsieh F.,

[illegible]

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QY 360 RDLFTASNDPLLRFLYLRDRFNTVRVQDTDWKELYRKRHHIQRKESKGRFVWMLLPST 419
Db 361 HDLLIASNDPLLRCLYLRDFDGTGVRGDTIDWKELYRKKHQRKHAQMRHAMFLPSA- 419
QY 420 HTIPIYPNLHRRPF-PSRLPPGIIGGEYDORPILPVYDPISSLIIPGPGTTPSQFPL 478
Db 420 HPFPCPIPVYPRAYLPTSLPGLPIIGGEYDERPILPSVGDPTVTSILPRPGELPQGRPL 479
QY 479 RRPDPVGLPGNPLPGRGGNDRFPFRPSGRGPTDGRLSFM 522
Db 480 RRPDPVGLPGHSLPGLPNNRFPFRPSGRSADSRLLPFL 523

RESULT 4
Q6Y0L7 PRELIMINARY; PRT; 361 AA.
AC Q6Y0L7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE F-box only protein 7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_
RP SEQUENCE FROM N.A.
RA Emaru M.G., Kim H.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194289; AAP83452.1; -.
DR EMBL; AY194288; AAP83452.1; JOINED.
DR InterPro: IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; F-box; 1.
DR PROSITE; PS0181; FBOX; 1.
FT NON TER 1
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0292833884 CRC64;

Query Match 47.0%; Score 1295; DB 2; Length 361;
Best Local Similarity 65.6%; Pred. No. 6.9e-78;
Matches 246; Conservative 47; Mismatches 62; Indels 20; Gaps 4;

QY 153 DNAHAEGTGFVPSPEMLCSVEGVPHSLTLYQSDCSDANDALIVLHLLMESGY 212
Db 2 EDVDLEEGTGVSPPEMLCSEADGEIPLSLVILSAECTSATDALIVLHLLMETGY 61

QY 213 IPQGTAKALSMPKWKLVGVYKLYQYMHPLCGSSATLTCPVPLGNLVVNAATLKINNEIR 272
Db 62 VPQGTAKAVSMPEKWRGNGVYKLYQYHPLCEGSAGLTCPVPLGNLVVNAATLKINREIK 121

QY 273 SVKRIQLLPESITCKELGENTVANIYKDLKLSRLFKDQLVYPLAFTQALNLPDVVGL 332
Db 122 GVKRIQLLPASVFCQE-PEKVAGVYKDLKLSRLFKDQLVYPLAFTQALNLPDVVGL 180

QY 333 VVLPLELKLRIFLDLVRSVLSAVCRDLFTASNDPLLRFLYLRDRFNTVRVQDTDW 392
Db 181 VVLPLELKLRIFLDLVRSVLSAVCRDLFTASNDPLLRFLYLRDRFNTVRVQDTDW 392

QY 393 KELYRKRHHIQRKESKGRFVWMLLPSTHTIPFPNPLHRRPFPPSSRLP-----PGIIGE 447
Db 228 SELYKKKLQKKEALRRH-MFLPTTPHPHPHPNPFYSPFPNPFPPNPFPPNPFPPNPF 286

QY 448 YQORTPLPVGDPIISLIIPGGETTSQFPPLPRPRDPVGLPGNPLPGRGGNDRPFP 507
Db 287 YGERPTLLYIGDPIINSLIPGGEAQCFPPRPHFDPIGSLGANCPTLPGRAGPSDRPFP 346

QY 508 RPSRGPTDGRLSFM 522
Db 347 RPSRGPTDVRRAFI 361

RESULT 5
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Q6DE59 PRELIMINARY; PRT; 478 AA.
ID Q6DE59;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Fbox7-prov protein.
GN Name=fbox7-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]_
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]_
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077283; AAH77283.1; -.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001226; Flavodoxin.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS0181; FBOX; 1.
DR PROSITE; PS0201; FLAVODOXIN; UNKNOWN 1.
DR PROSITE; PS0201; FLAVODOXIN; UNKNOWN 1.
SQ SEQUENCE 478 AA; 53251 MW; 8C12F01E32C1873F CRC64;

Query Match 40.8%; Score 1125; DB 2; Length 478;
Best Local Similarity 47.5%; Pred. No. 2e-66;
Matches 251; Conservative 74; Mismatches 147; Indels 56; Gaps 14;

QY 1 MRLRVLLKRPWLPVEPTEPTLHLSHLRLSLCTWGYSSNTFTITLVNKPDLTGD 60
Db 1 MRLRVKRPVSRLEAEQPTGLDRSLKSLSVTLPSLGSYSAETHFTITLNGKDALTE 60

QY 61 ETLSAGYIVSGDLICLILOD--DIPAPNIPSTDSHSSLNQNEQPSLATSSNOTSMODE 118
Db 61 TTLESAGIISGDLIVLLPDPQLAPPAPERD-PRCELEDPTQP-----CSTANK 111

QY 119 QPSDSFGQAAQSGVWVNDSDMLGSPNFSESIONAHMAEGTGYPs-EPMLCSSEV 177
Db 119 QPSDSFGQAAQSGVWVNDSDMLGSPNFSESIONAHMAEGTGYPs-EPMLCSSEV 177
```

Db	112	RP-----KGHADNEGA-----GAMPQAEAPSLDDVAM--EGQLSGPAWEVMLCSRAVDG	159
Qy	178	QVPHSLETLYQSADCSANDALIVLHLLMLSEGYIPQGTAKALSMPEKWLKSGVYKLG	237
Db	160	KIPHSLEVLYQTASCSASTDAFIVIVHLLMLETYLHKGAETKALCWPDRWRSGGAYRLH	219
Qy	238	YMHPLCEGSSATLTCVPLGNLIVVNATLKINNETRSVKRLQLLPSPICEKLGENVANI	297
Db	220	YTHPLCAEVSATVCLPMPGKLVINATWKINSEKSVRKQLLTNSYISYPETDNNVASV	279
Qy	298	YKDLOKLSRLFKDQQLVYVLLAFTROALNLPDVFGLVPLLELKLRIFFLLDVRSLVLSLSA	357
Db	280	YKDLOKLSQFQKQVAYPLLAAARQVNLDPVGLVLPPELKLRIFFLLDIIRLSLNSA	339
Qy	358	VCRDLFTASNDPLLNRFLYLRDFRDNTVRVQDTPWKELYRKRHIQRKESPKGRFV---	ML 414
Db	340	TKCELLADTDDPSLRKFLCIRDFRNSLPRLNLTGTDWKXLYKEFKQKMD--RNFVRVRQFL	397
Qy	415	LPSSHTHTPPYNPPLHPRFPSSRLPGCIIGCEVDQRPTLPYVGDDPISLLIPGCGTTPSQ	474
Db	398	PPRNPAPHYEPYEN-VFP---PDINYPGCIIGDVDQRPPFPFV-----NPTH 440	
Qy	475	FPPLRPDPVCPGLCPNPILPGRGGPNDRFPFPSPRGRPTDGRLSFM 522	
Db	441	LNP-----FKVTLFPSENDPSIPGSSG-----LRPSRGRGLDIRRGFI 478	
RESULT 6			
Q9ZUB8			
ID	Q9ZUB8	PRELIMINARY;	PRT; 475 AA..
AC	Q9ZUB8;		
DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)	

RESULT 6

Q9ZUB8		PRT;	475 AA.
ID	Q9ZUB8	PRELIMINARY;	
AC	Q9ZUB8;		
DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	
DE	05-JUL-2004	(TREMBLrel. 27, Last annotation update)	
DE	F508_33 protein (Atlg23780/F508_31).		
GN	Name=F508_33;		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,		
RA	Li J., Kremensskaia I., Luros J., Altafi H., Gonzalez A.; Araujo R.,		
RA	Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L.,		
RA	Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,		
RA	Ecker J.R., Federspiel N.A., Theologis A.;		
RL	Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.		

[illegible]

RESULT 7

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RESOUR
ID      Q8GV6      PRELIMINARY;      PRT;      776 AA.
AC      Q8GV6;
DT      01-MAR-2003 (T-EMBLrel. 23, Created)
DT      01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT      01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE      Hypothetical protein OJ1017C11.10.
DN      Names:OJ1017C11.10;
GN      Oryza sativa (japonica cultivar-group).
OS      Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC      Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=39947;
[1]
RN
RP      SEQUENCE FROM N.A.
RA      Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
RA      Collura K.;
RL      Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RC      -/- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR      EMBL; AC131517; AAC00689.1; -.
DR      Gramene; Q8GV6; -.

```


QY 164 YSEPMCLSESVEGQVPHSLETLYQADSCDANDALIVLIHLLMLESYGIPQGTAKA-L 222
DB 123 -----SDTVR-----ADDEENES-----PAETDLQAO 146
QY 223 SNPEKWLKSGVLYQYMHPLCEG-SSATLTCVPL-----GNLIVVNATLKINNE----- 270
DB 147 QM-----FRAQWMPFELAPGVSSNLENRPCRARGSLQKTSADTKGQOEQAEEKA 197
QY 271 -----IRSV-----KRLQLPE-----SPICKEKLGENVANIY-----KDLQ 302
DB 198 RELFUKAVEEQNGALYRAIKFYRRAMQLVPDIEFKITYTRSPDGVGNSYIEDNDDDS 257
QY 303 KLSRL---FKQOLVYPLLAFTRAQALNL--PDV-----FGLVVLPLELKLRIPL-----LD 348
DB 258 KWADLLSYFQQ-----LTFQESVLKLCQPELESSQIHISVLPMEVLYIFRWVVSDDL 312
QY 349 VRSVLSLSAVCHDLFTASNDPLLWRFLYLDRFRONTVR-VQDTWKELYRKHIOQKESPKGRFVMLLPS 407
DB 313 LRSLEQLSLVCRGFYICARDPEIWRACLKVMGRSCIKLVPYTSWREMFLE-----P 365
QY 408 KGRFVMLLPSPT-----HTIPFPNPLHPRPSPSSRLPFCIIIGGEYDQ 450
DB 366 RVRFPGVIVISKTYIROQESQLDGFYRAWHQVEYY---RYIRFFPDGHV----- 411
QY 451 RPTLPYVGDPISSILPGCGETSPQFPPLRPR 481
DB 412 -----MMLTTPPEPQSIIVPLRTR 430

RESULT 11

ID Q6PKH7 PRELIMINARY; PRT; 403 AA.
AC Q6PKH7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE FBX09 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
ET and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; SC000650; AA000650.2; -;
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.

DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 403 AA; 47361 MW; 1AAALF46C31315BB CRC64;
Query Match 5.2%; Score 144; DB 2; Length 403;
Best Local Similarity 23.1%; Pred. No. 0.21;
Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;
QY 233 VKLQYMHPLCEG-SSATLTCVPL-----GNLIVVNATLKINNE-----IRSV-- 274
DB 1 MFRQWMPFELAPGVSSNLENRPCRARGSLQKTSADTKGQOEQAEEKARELFLKAVEE 60
QY 275 -----KRLQLPE-----SPICKEKLGENVANIY-----KDLQKLSRL-----FK 309
DB 61 EQNGALYEAIFKYRRAMQLVPDIEFKITYTRSPDGVGNSYIEDNDDDSKWADLLSYFQ 120
QY 310 DQVYVPLLAFTRAQALNL--PDV-----FGLVVLPLELKLRIPL-----LDVRSVLSLSAV 358
DB 121 QQ-----LTFQESVLKLCQPELESSQIHISVLPMEVLYIFRWVVSDDLRLSLQSLIV 175
QY 359 CRDLFTASNDPLLWRFLYLDRFRONTVR-VQDTWKELYRKHIOQKESPKGRFVMLLPS 417
DB 176 CRGFYICARDPEIWRACLKVMGRSCIKLVPYTSWREMFLE-----PRVFPDGVIVIS 228
QY 418 ST-----HTIPFPNPLHPRPSPSSRLPFCIIIGGEYDQRTLPYVGD 460
DB 229 KTYIROQESQLDGFYRAWHQVEYY---RYIRFFPDGHV----- 264
QY 461 ISSILPGCGETSPQFPPLRPR 481
DB 265 --MMLTTPPEPQSIIVPLRTR 283

RESULT 12

ID Q9NT57 PRELIMINARY; PRT; 437 AA.
AC Q9NT57;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFP434C0118.
GN Name=DKFP434C0118;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137520; CAB70786.2; -;
KW Hypothetical protein.
SQ SEQUENCE 437 AA; 51135 MW; AF7DCF6AD4F4035E CRC64;

Query Match 5.2%; Score 144; DB 2; Length 437;
Best Local Similarity 23.1%; Pred. No. 0.24;
Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;
QY 233 VKLQYMHPLCEG-SSATLTCVPL-----GNLIVVNATLKINNE-----IRSV-- 274
DB 35 MFRQWMPFELAPGVSSNLENRPCRARGSLQKTSADTKGQOEQAEEKARELFLKAVEE 94
QY 275 -----KRLQLPE-----SPICKEKLGENVANIY-----KDLQKLSRL-----FK 309
DB 95 EQNGALYEAIFKYRRAMQLVPDIEFKITYTRSPDGVGNSYIEDNDDDSKWADLLSYFQ 154
QY 310 DQVYVPLLAFTRAQALNL--PDV-----FGLVVLPLELKLRIPL-----LDVRSVLSLSAV 358
DB 155 QQ-----LTFQESVLKLCQPELESSQIHISVLPMEVLYIFRWVVSDDLRLSLQSLIV 209
QY 359 CRDLFTASNDPLLWRFLYLDRFRONTVR-VQDTWKELYRKHIOQKESPKGRFVMLLPS 417

Db 210 CRGFYICARDPEIWRLLACKWGRSCIKLVPTYSWREMFLEP-----PRVRFQGVYIS 262

QY 418 ST-----HTIPFFPNLHPFPSSRLPPGIIGGYDQRTPLPVGDP 460

Db 263 KTYIIRQGEQSLDGFYRAWHQVEYY---RYIRFFPDGHV-----298

QY 461 ISSLIPGCGETPSQPPPLRPR 481

Db 299 --MMLTTPPEQSIIVPLRLTR 317

RESULT 13

FBX9 HUMAN STANDARD; PRT; 447 AA.

AC Q9UK97; 075986; DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE F-box only protein 9.

GN Name=FBX9; Synonyms=FBX9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2003061; PubMed=10531037; DOI=10.1016/S0960-9822(00)80021-4;

RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.,

RT "A family of mammalian F-box proteins."

RL Curr. Biol. 9:1180-1182(1999).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;

RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,

RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,

RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainsworth R.,

RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,

RA Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,

RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,

RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,

RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,

RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,

RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,

RA Cullen K.M., Dhami P., Davies J., Dunn M., Earthrow M.E.,

RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,

RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,

RA Gilby L.M., Gillson C.J., Glithero R.J., Graham D.V., Grant M.,

RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hall K.S.,

RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,

RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,

RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,

RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,

RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,

RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,

RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLeay K.,

RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,

RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,

RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,

RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,

RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,

RA Squares S.I., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,

RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,

RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,

RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,

RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,

RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.,

RT "The DNA sequence and analysis of human chromosome 6."

RL Nature 425:805-811(2003).

RN [3]

RP SEQUENCE OF 121-447 FROM N.A.

RX MEDLINE=2003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;

RA Cenciarelli C., Chiau D.S., Guardavaccaro D., Parks W., Vidal M.,

RA Pagano M.;

RT "Identification of a family of human F-box proteins.";

RL Curr. Biol. 9:1177-1179(1999).

CC FUNCTION: Probably recognizes and binds to some phosphorylated

CC proteins and promotes their ubiquitination and degradation.

CC SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex

CC (By similarity).

CC SIMILARITY: Contains 1 F-box domain.

CC SIMILARITY: Contains 1 TPR repeat.

CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

EMBL; AF176704; AAF03704.1; --

DR EMBL; AL031178; CAA20122.1; --

DR EMBL; AF174597; AAF04518.1; --

DR Genew; HGNC:13588; FBX9.

DR GO; GO:0000151; C:ubiquitin ligase complex; NAS.

DR GO; GO:0004842; E:ubiquitin-protein ligase activity; NAS.

DR GO; GO:0016567; F:protein ubiquitination; NAS.

DR InterPro; IPR001810; F-box.

DR InterPro; IPR008945; Skp1_Skp2.

DR InterPro; IPR008941; TPR-like.

DR Pfam; PF00646; F-box; 1.

DR PROSITE; PS50181; FBOX; 1.

KW TPR repeat; UBI conjugation pathway.

FT REPEAT 94 127

FT DOMAIN 185 236 F-box.

SQ SEQUENCE 447 AA; 52329 MW; 2A88163DAB898D69 CRC64;

Query Match 5.2%; Score 144; DB 1; Length 447;

Best Local Similarity 23.1%; Pred. No. 0.24;

Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;

QY 233 VYKLVYHPLCEG--SSATLTCVPL-----GNLTIVNATLKINNE-----IRSV-- 274

Db 45 MFRQWMEFAPGVSSNNLENRPCRARGSLQKTSADTKGQKQKAEKARELFKAVSE 104

QY 275 -----KRLQLPE-----SFICKEKLGENVANIY-----KDLQKLSRL---PK 309

Db 105 EQNGALYBAIKFYRRAMQLVPDIEFKITVTRSPDGVGVNSYIEDNDDSKMALLSYFQ 164

QY 310 DQLVYPLLAFTQALNL--PDV-----FGLVVLPLEKLKRIPL-----LDVRSVLSLSAV 358

Db 165 QQ-----LTFQESVLKLCQPELESSQIHISVLPMELVMYIFRWVSVSSDLDRSLQSLV 219

QY 359 CRDLFTASNDPLLRFLYLRDFRDNVTR--VQDTPDKELYRKHIQRKESPKGRFVMLLPS 417

Db 220 CRGFYICARDPEIWRLLACKWGRSCIKLVPTYSWREMFLEP-----PRVRFQGVYIS 272

QY 418 ST-----HTIPFFPNLHPFPSSRLPPGIIGGYDQRTPLPVGDP 460

Db 273 KTYIIRQGEQSLDGFYRAWHQVEYY---RYIRFFPDGHV-----308

QY 461 ISSLIPGCGETPSQPPPLRPR 481

Db 309 --MMLTTPPEQSIIVPLRLTR 327

RESULT 14

Q7ZTY2 PRELIMINARY; PRT; 356 AA.

ID Q7ZTY2

AC Q7ZTY2

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Similar to F-box only protein 32.

GN ORFNames=zgc:56479;

```

OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC052112; AAHS2112.1; -.
DR ZFIN; ZDB-GENE-040426-1040; zgc:56479.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 356 AA; 41897 MW; 21FE8A1E90B45DC2 CRC64;

Query Match          5.0%; Score 138.5; DB 2; Length 356;
Best Local Similarity 27.1%; Pred. No. 0.41;
Matches 62; Conservative 31; Mismatches 75; Indels 61; Gaps 11;

QY 230 LSGVYKLYMHPLCEGSSATLTCVPLGNLI--VNNATLKINNEIRSVKRLQLLPESFICK 287
Db 138 LSGVAQKNY-----NILERVQKVLDDQNVPRIKELLQTLVASLCS 180

QY 288 --EKLGENV-----ANIYKDLKLSRLFKDQLVPLLAFTQAALNLPVFG-- 331
Db 181 LVQDMGKSVLGNINIWHRMENILQWQQLDNI-----QINRPKNTGMT 225

QY 332 LVLPLEKLRTF-RLLDVRSLSLSAVCRDLFTASNDPLLRFLYLRDFRDNVTR---- 386
Db 226 LLELPVSLQNLIMQRLSDGRDLVSLGQVCPDLMLTEBRLMKLQCHFTDRQIRKRLM 285

QY 387 VOD---TDWKLYKRKHQKESPKGRFVMLLPSSHTT-IPFPNPLHP 431
Db 286 VSDKGQLEWKNYFK--LCRCYPKHEQYSDTLQFCTHCHILFWKDTDHP 332

RESULT 15
Q8VDY6 PRELIMINARY; PRT; 436 AA.
AC Q8VDY6;
DC 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fbxo9 protein.

```

```

GN Name=Fbxo9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC020074; AAH20074.1; -.
DR MGD; MGI:1918788; Fbxo9.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS0181; FBOX; 1.
SQ SEQUENCE 436 AA; 50672 MW; 3479C6C144A26805 CRC64;

Query Match          4.9%; Score 135; DB 2; Length 436;
Best Local Similarity 22.7%; Pred. No. 0.93;
Matches 57; Conservative 41; Mismatches 67; Indels 86; Gaps 11;

QY 275 KRLQLLP-----SFICKEKLGENVANIY---KDLQKLSRLFKDQLVPLLAFTQAALNL 326
Db 108 RAMQLVPDIEFKIYTRSPDGDGSGVYIENEDASKVA-----DLSYFQQLTL 158

QY 327 -----PDV---FGLVVLPLELKLRIPL-----LDVRSVLSLSAVCRDLFTASND 368
Db 159 QESVLKLCQPELETSTQTHISVLPWEVLMIYFRVWVSSDLRLSLQLSILVCRGFYICARD 218

QY 369 PLLWRFLYLRDFRDNVTR-VQDTWKELYKRKHQKESPKGRFVMLLPST----- 419
Db 219 FEIWRACLKVGWGRSCMKLVFVYASWREMFLEPR-----PRVRFDDGVVISKTYIRQGEQ 271

QY 420 -----HTIPFPNPLHPRPSPSSRLPFGIIGGEYDQRPRTLPHYGDPISSLIPGCGE 470
Db 272 SLDGFYRAHWQVEYY---RYWRFPDGHV-----MMLTPEE 305

QY 471 TPSQFPPLRPR 481
Db 306 PPSIVPLRLTR 316

Search completed: July 19, 2005, 20:19:50
Job time : 174 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2005, 20:06:57 ; Search time 166 Seconds
(without alignments)
1216.198 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 2754

Sequence: 1 MRLRVLKRTWPLEVPETE.....DRPPFRPGRPTDGLSLFM 522

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A. Geneseq 16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2748	99.8	522	ADA57283	Human sec
2	2748	99.8	522	ADA41163	Human sec
3	2748	99.8	522	ABR47958	Human sec
4	2748	99.8	522	ADC74366	Human sec
5	2744	99.6	522	AAB35161	Human Skp
6	2744	99.6	522	ABM82342	Tumour-as
7	2510	91.1	591	AAW68521	Human RIP
8	2489	90.4	482	AAI783047	Human F-b
9	2489	90.4	482	AAO22452	Human F-b
10	2448.5	88.9	607	AAU32109	Human pol
11	2404	87.3	462	ABB90109	Human sec
12	2404	87.3	462	ADA57586	Human sec
13	2404	87.3	462	ADA41482	Human sec
14	2404	87.3	462	ABR48139	Human sec
15	2404	87.3	462	ADC74596	Human sec
16	2270	82.4	443	AAAB35160	Human Skp
17	2086.5	75.8	549	ABG18510	Novel hum
18	1527	55.4	317	ABR90108	Human pol
19	1328	45.0	231	ADJ68946	Human hea
20	1086	39.4	221	ADA54155	Human pro
21	714	25.9	174	ADA57587	Human sec
22	714	25.9	174	ADA41483	Human sec
23	714	25.9	174	ABR48140	Human sec
24	714	25.9	174	ADC74597	Human sec
25	714	25.9	175	AAY41397	Human sec

ALIGNMENTS

RESULT 1

ADA57283

ID ADA57283 standard; protein; 522 AA.

XX AC ADA57283;

XX DT 20-NOV-2003 (first entry)

XX DE Human secreted protein #566.

XX KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;

XX KW cytostatic; cerebroprotective; neuroprotective; nootropic;

XX KW cardiovascular; antiarteriosclerotic; gene therapy;

XX KW human secreted protein; immune disorder; inflammation;

XX KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;

XX KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;

XX KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;

XX KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;

XX KW triple helix formation; antisense gene therapy; forensic biology.

XX OS Homo sapiens.

XX PN WO2002102994-A2.

XX PD 27-DEC-2002.

XX PF 19-MAR-2002; 2002WO-US008278.

XX PR 21-MAR-2001; 2001US-0277340P.

XX PR 13-JUL-2001; 2001US-0306171P.

XX PR 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2003-167512/16.

XX N-PSDB; ADA56387.

XX PT New human secreted polypeptides and polynucleotides, useful for

XX PT diagnosing, treating or preventing e.g. immune disorders, inflammatory

XX PT conditions, respiratory disorders, cancers, CNS disorders, or

XX PT neurodegenerative disorders.

XX PS Claim 13; SEQ ID NO 1473; 1754pp; English.

XX CC The invention relates to 592 new human secreted polypeptides useful for

XX CC diagnosing, treating or preventing e.g. immune disorders, inflammatory

Aau32107 Novel hum
Abo54274 Human gen
Aay87356 Human sig
Abg18509 Novel hum
Abg18509 Novel hum
Aau32108 Novel hum
Abo59882 Human gen
Aag29404 Arabidops
Aao28054 F-box mot
Aao22459 Human F-b
Aay02272 A F-box p
Aao08044 Human F-b
Aae39652 Human F-b
Aad68977 Human F18
Aay02273 A F-box p
Aao08045 Mouse F-b
Aae39653 Mouse F-b
Aad68979 Mouse F18
Aag29406 Arabidops
Aag29405 Arabidops

CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.6e-239;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLLKRTWPLEVPETETPLGHLRSHLRSLCTGWGYSNTRFTTLNPKDPLTGD 60
Db 1 MRLRVLLKRTWPLEVPETETPLGHLRSHLRSLCTGWGYSNTRFTTLNPKDPLTGD 60
Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDTSEHSSIQNNBOPSLATSSNQTSMQDSQP 120
Db 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDTSEHSSIQNNBOPSLATSSNQTSMQDSQP 120
Qy 121 SDSFQGAQAQGVWDDSMGLPQSFQFEAESIQDNNAHMAEGTGFYSPMLCSVESVEGQVP 180
Db 121 SDSFQGAQAQGVWDDSMGLPQSFQFEAESIQDNNAHMAEGTGFYSPMLCSVESVEGQVP 180
Qy 181 HSLETLYQSADCDANDALIVLIHLLMESGYIPOGTEAKALSMPEKWLKSGVYKLYMH 240
Db 181 HSLETLYQSADCDANDALIVLIHLLMESGYIPOGTEAKALSMPEKWLKSGVYKLYMH 240
Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFTCKEKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFTCKEKLGENVANIYKD 300
Qy 301 LQKLSRLFKDQVYVYLLAFTQALNLPDVGVLVPLLELKLIRFLDLVRSVLSLSAVCR 360
Db 301 LQKLSRLFKDQVYVYLLAFTQALNLPDVGVLVPLLELKLIRFLDLVRSVLSLSAVCR 360
Qy 361 DLFTASNDPLLRFLYLRDPRNTVRVQDTWKELYRKRHTQRKESPKGRFVMLLPSSHT 420
Db 361 DLFTASNDPLLRFLYLRDPRNTVRVQDTWKELYRKRHTQRKESPKGRFVMLLPSSHT 420
Qy 421 TIFPFPNPLHPPFPSSRLPGCIIGGEYDQRTPLPVGDPITSLIPGPGEPSPQFPPLRP 480
Db 421 TIFPFPNPLHPPFPSSRLPGCIIGGEYDQRTPLPVGDPITSLIPGPGEPSPQFPPLRP 480
Qy 481 RFDVPGVPLPGPNPILPGRGGPNDRFPFRPSGRPTDGRLSFM 522
Db 481 RFDVPGVPLPGPNPILPGRGGPNDRFPFRPSGRPTDGRLSFM 522

RESULT 2
, ADA41163

ID ADA41163 standard; protein; 522 AA.
XX
AC ADA41163;
XX
DT 20-NOV-2003 (first entry)
XX Human secreted protein.
DE
XX Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnery; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
XX WO2002102993-A2.
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2003-175238/17.
XX
XX New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 1; SEQ ID NO 1545; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.6e-239;

		Matches	521;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	MRLRVLLKRTWP	LEVPETPTLGH	RLSHLRSL	LLCTWGY	SNTRFTT	TLN	KDPL	TGDE	60	
Db	1	MRLRVLLKRTWP	LEVPETPTLGH	RLSHLRSL	LLCTWGY	SNTRFTT	TLN	KDPL	TGDE	60	
QY	61	ETLASYGIVSGD	LICLILODDI	PAPNIP	SSDSEHSS	LQNNQPS	LATSS	NTQ	SMQDEQ	120	
Db	61	ETLASYGIVSGD	LICLILODDI	PAPNIP	SSDSEHSS	LQNNQPS	LATSS	NTQ	SMQDEQ	120	
QY	121	SDSFGQAAQSG	VWDDSM	LGPSQNF	AEESIQD	NAHMAEGT	GFYSE	PMLC	SESV	EGQVP	180
Db	121	SDSFGQAAQSG	VWDDSM	LGPSQNF	AEESIQD	NAHMAEGT	GFYSE	PMLC	SESV	EGQVP	180
QY	181	HSLETLYQSAD	CSDANDAL	IVLHLL	MLES	GVIP	PGT	EAKAL	SMPEK	WKL	SGVYK
Db	181	HSLETLYQSAD	CSDANDAL	IVLHLL	MLES	GVIP	PGT	EAKAL	SMPEK	WKL	SGVYK
QY	241	PLCEGSSATL	TCVPLGNL	IVVNAT	LKINNE	IRSVK	RLQL	LPES	FICKE	KL	GENVANI
Db	241	PLCEGSSATL	TCVPLGNL	IVVNAT	LKINNE	IRSVK	RLQL	LPES	FICKE	KL	GENVANI
QY	301	LQKLSRLFKD	QLVYPL	LAFT	QALN	LPDV	FG	LV	PLEL	KL	RI
Db	301	LQKLSRLFKD	QLVYPL	LAFT	QALN	LPDV	FG	LV	PLEL	KL	RI
QY	361	DLFTASNDP	LLWRFL	YL	RD	FRD	NT	VR	VD	TW	KEL
Db	361	DLFTASNDP	LLWRFL	YL	RD	FRD	NT	VR	VD	TW	KEL
QY	421	TIPFPNPLH	PRPFSS	RLPG	II	IG	EYD	Q	R	P	T
Db	421	TIPFPNPLH	PRPFSS	RLPG	II	IG	EYD	Q	R	P	T
QY	481	RFPDVG	PLPG	PNP	IL	PG	RG	PN	DR	PP	PS
Db	481	RFPDVG	PLPG	PNP	IL	PG	RG	PN	DR	PP	PS
RESULT 3											
ID	ABR47958	standard; protein; 522 AA.									
XX	ABR47958										
AC	ABR47958										
DT	12-JUN-2003	(first entry)									
DE	Human	secreted protein, SEQ ID 849.									
KW	Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerable; antiinflammatory; neurotropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.										
OS	Homo sapiens.										
PN	WO200295010-A2.										
XX	28-NOV-2002.										
PF	19-MAR-2002; 2002WO-US009785.										
PR	21-MAR-2001; 2001US-0277340P.										
PR	19-JUL-2001; 2001US-0306171P.										
PR	13-NOV-2001; 2001US-0331287P.										
XX	(HUMA-) HUMAN GENOME SCI INC.										
XX	Rosen CA, Ruben SM;										
XX	WPI; 2003-129429/12.										
PT	Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular										

PT	disorders such as arrhythmia.
XX	Claim 13; SEQ ID NO 849; 1881pp; English.
XX	The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, renal disorders, proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in Alzheimer's disease and Parkinson's neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 522 AA;
QY	Query Match: 99.8%; Score 2748; DB 6; Length 522;
Db	Best Local Similarity 99.8%; Pred. No. 5.6e-239;
QY	Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1	MRLRVLLKRTWP
1	MRLRVLLKRTWP
61	ETLASYGIVSGD
61	ETLASYGIVSGD
121	SDSFGQAAQSG
121	SDSFGQAAQSG
181	HSLETLYQSAD
181	HSLETLYQSAD
241	PLCEGSSATL
241	PLCEGSSATL
301	LQKLSRLFKD
301	LQKLSRLFKD
361	DLFTASNDP
361	DLFTASNDP
421	TIPFPNPLH
421	TIPFPNPLH
481	RFPDVG
481	RFPDVG
RESULT 4	
ADC74366	

ID AD4366 standard; protein; 522 AA.
AC AD4366;
XX
XX
XX 01-JAN-2004 (first entry)
XX
XX Human secreted protein - SEQ ID 999.
XX
XX antianemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatologic; nephrotropic; antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
XX
XX Homo sapiens.
XX
XX WO2003038063-A2.
XX
XX 08-MAY-2003.
XX
XX 19-MAR-2002; 2002WO-US008277.
XX
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
PI
XX
XX WPI; 2003-430516/40.
DR N-PSDB; ADC73751.
XX
XX New human secreted polypeptide for diagnosing, preventing or treating
PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT atherosclerosis).
XX
XX Claim 16; SEQ ID NO 999; 2272pp; English.
PS
XX The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting
CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC The current sequence is that of the human secreted protein of the
CC invention.
XX
XX Sequence 522 AA;
SQ

Query Match 99.8%; Score 2748; DB 7; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.6e-239;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 MELRLVLLKRTWPLEVPEPETEPTLGLHRLSHLSLLCTWGYSSNTRFTITLNYKDLTGDG 60
1 MELRLVLLKRTWPLEVPEPETEPTLGLHRLSHLSLLCTWGYSSNTRFTITLNYKDLTGDG 60
61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDTSEHSSLQNNQEPSLATSSNQTSMQDEQP 120

Db 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDTSEHSSLQNNQEPSLATSSNQTSMQDEQP 120
QY 121 SDSFQQAQSGVWDDSMGLGFSQNFEAESIQDNAHMAEGTGTFYSEPMLCSESVEGQVP 180
Db 121 SDSFQQAQSGVWDDSMGLGFSQNFEAESIQDNAHMAEGTGTFYSEPMLCSESVEGQVP 180
QY 181 HSLETLYOSADCSANDALIVLIHLMLLESGVYIPGTEAKALSMPEKWKLSGVYKLOYMH 240
Db 181 HSLETLYOSADCSANDALIVLIHLMLLESGVYIPGTEAKALSMPEKWKLSGVYKLOYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300
QY 301 LOKLSRLFKDQIVYPLLAFTQAALMLPDVGLVLPLELKLRIFRLLDVRSVLSAVCR 360
Db 301 LOKLSRLFKDQIVYPLLAFTQAALMLPDVGLVLPLELKLRIFRLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLLRFLYLRDRDNTVRVODTDWKELYRKRHIQKESPKGRFVMLLPSSSTH 420
Db 361 DLFTASNDPLLRFLYLRDRDNTVRVODTDWKELYRKRHIQKESPKGRFVMLLPSSSTH 420
QY 421 TIPFYPNLHPRPPSPSSRLPGIIGGEYDQRPPTLPYVGDPISLLIPGCGTSPQFPPLRP 480
Db 421 TIPFYPNLHPRPPSPSSRLPGIIGGEYDQRPPTLPYVGDPISLLIPGCGTSPQFPPLRP 480
QY 481 RFDVPGPLPGNPILPGRGGNDPRFPSPGRPTDGLSPM 522
Db 481 RFDVPGPLPGNPILPGRGGNDPRFPSPGRPTDGLSPM 522

RESULT 5
AAB35161
ID AAB35161 standard; protein; 522 AA.
XX
AC AAB35161;
XX
DT 09-APR-2001 (first entry)
XX
DE Human Skpl-associated F-box protein-1 SAF-beta SEQ ID NO: 10.
XX
KW Human; protein degradation; siah-mediated degradation protein; SMDP;
KW SCF-complex protein; SCP; siah-1alpha; siah-1 interacting protein; SIP;
KW Skpl-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division;
KW Skpl-associated destruction-box protein; inflammatory disease.
XX
OS Homo sapiens.
PN WO2000077207-A2.
XX
PD 21-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US015873.
XX
XX 11-JUN-1999; 99US-00330517.
XX
PA (BUEN-) BURNHAM INST.
XX
PI Reed JC, Matsuzawa S;
XX
DR WPI; 2001-071273/08.
DR N-PSDB; AAC67285.
XX
XX Siah-Mediated Degradation Protein, useful for drug screening, for
PT therapeutic applications and for functional genomics.
XX
PS Claim 15; Page 107-108; 121pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC several siah-mediated degradation proteins and SCF-complex proteins.
CC These are designated Siah-1alpha, Siah-1 interacting protein (SIP), which
CC encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skpl-


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CC associated F-box protein-lalpha and beta and -2 (SAF-lalpha, SAF-lbeta
CC and SAF-2) and Skp1-associated destruction-box protein (SAD). The
CC proteins and their coding sequences are useful in the diagnosis and
CC treatment of cancers, disorders where too little cell division occurs
CC such as bone marrow aplasia, immunodeficiencies and inflammatory
CC diseases including sepsis, fibrosis, arthritis and graft versus host
CC disease
XX
XX
SQ Sequence 522 AA;

Query Match          99.6%; Score 2744; DB 4; Length 522;
Best Local Similarity 99.6%; Pred. No. 1.3e-238;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLRVLRLKRTWPLEVPETPTLGLHRLSHLRLSLCTWGYSSNTFTITLNYKDPDPTGDE 60
DB 1 MRLRVLRLKRTWPLEVPETPTLGLHRLSHLRLSLCTWGYSSNTFTITLNYKDPDPTGDE 60
QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
DB 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
QY 121 SDSFOGQAQAGVWDDSMGLGFSQNFEAESIODNAHMAEGTGYFSEPMLCSESVEGQVP 180
DB 121 SDSFOGQAQAGVWDDSMGLGFSQNFEAESIODNAHMAEGTGYFSEPMLCSESVEGQVP 180
QY 181 HSLETLYQSADCSANDALIVLIHLMLSEGYIPQGTAKALSMPEKWLKSGVYKLYQYMH 240
DB 181 HSLETLYQSADCSANDALIVLIHLMLSEGYIPQGTAKALSMPEKWLKSGVYKLYQYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKNNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVVNATLKNNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
QY 361 DLFTASNDPLLWRFLYLRDRNTVVRQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
DB 361 DLFTASNDPLLWRFLYLRDRNTVVRQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
QY 421 TIPFPYVPLPGRGPNDRPFRPSRGRPTDGRLSFM 522
DB 421 TIPFPYVPLPGRGPNDRPFRPSRGRPTDGRLSFM 522
QY 481 RPDVGPPLPGRGPNDRPFRPSRGRPTDGRLSFM 522
DB 481 RPDVGPPLPGRGPNDRPFRPSRGRPTDGRLSFM 522

RESULT 6
ID ABM82342
XX ABM82342 standard; protein; 522 AA.
AC ABM82342;
XX
XX
XX 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO3271, SEQ.6018.
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW gene therapy; cytostatic.
XX
XX Homo sapiens.
XX
XX WO2004030615-A2.
XX
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PD 15-APR-2004.
XX 29-SEP-2003; 2003WO-US028547.
XX 02-OCT-2002; 2002US-0414971P.
XX (GETH ) GENENTECH INC.
XX Wu TD, Zhang Z, Zhou Y;
XX WPI; 2004-347921/32.
XX N-PSDB; ACN40919.
XX New tumor-associated antigenic target polypeptides and nucleic acids,
XX useful in preparing a medicament for treating or detecting a
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX prostate cancer or tumor.
XX Claim 12; SEQ ID NO 6018; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
XX polypeptides, and their related nucleic acids. The TAT polypeptides are
XX overexpressed in cancer tissues compared to normal tissues, and may thus
XX serve as effective targets for the diagnosis and treatment of cancer in
XX mammals. The invention also relates to nucleic acid and polypeptide
XX sequences at least 80% identical to the TAT nucleic acids and
XX polypeptides; expression vectors and host cells comprising a TAT nucleic
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
XX TAT polypeptide; and methods and compositions for the treatment or
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
XX antibodies, antagonists, binding molecules and compositions are useful
XX for diagnosing or treating a cell proliferative disorder associated with
XX increased TAT expression, particularly cancers such as breast cancer,
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
XX cancer, pancreatic cancer, cervical cancer, cancers of the central
XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be
XX used as hybridisation probes, in chromosome and gene mapping, in
XX chromosome identification and in gene therapy. The present sequence
XX represents a TAT polypeptide of the invention
XX
XX Sequence 522 AA;

Query Match          99.6%; Score 2744; DB 8; Length 522;
Best Local Similarity 99.6%; Pred. No. 1.3e-238;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLRVLRLKRTWPLEVPETPTLGLHRLSHLRLSLCTWGYSSNTFTITLNYKDPDPTGDE 60
DB 1 MRLRVLRLKRTWPLEVPETPTLGLHRLSHLRLSLCTWGYSSNTFTITLNYKDPDPTGDE 60
QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
DB 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
QY 121 SDSFOGQAQAGVWDDSMGLGFSQNFEAESIODNAHMAEGTGYFSEPMLCSESVEGQVP 180
DB 121 SDSFOGQAQAGVWDDSMGLGFSQNFEAESIODNAHMAEGTGYFSEPMLCSESVEGQVP 180
QY 181 HSLETLYQSADCSANDALIVLIHLMLSEGYIPQGTAKALSMPEKWLKSGVYKLYQYMH 240
DB 181 HSLETLYQSADCSANDALIVLIHLMLSEGYIPQGTAKALSMPEKWLKSGVYKLYQYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKNNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVVNATLKNNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
QY 301 LQKLSRLFKDQVLPPLAFTRAQALNLPDVFGLVLPLEKLRIFRLLDVRVSLSAVCR 360
DB 301 LQKLSRLFKDQVLPPLAFTRAQALNLPDVFGLVLPLEKLRIFRLLDVRVSLSAVCR 360
QY 361 DLFTASNDPLLWRFLYLRDRNTVVRQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
DB 361 DLFTASNDPLLWRFLYLRDRNTVVRQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
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Db	361	DLFTASNDPLLRFLYLDRFRDNTVRVQTDWKELYRKHHIQRKESPKGRFVMLLPSSTH	420
Qy	421	TTPPEVNPPLHPPSPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP	480
Db	421	TTPFPNPPLHPPFPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP	480
Qy	481	REFDPVGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM	522
Db	481	REFDPVGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM	522
RESULT 7			
AAW68521	AAW68521 standard; protein; 591 AA.		
XX	AC	AAW68521;	
XX	DT	25-JAN-1999 (first entry)	
XX	DE	Human RIP-associated protein.	
XX	XX	Human; RIP-associated protein; RAP; primer; PCR; amplification; probe; hybridisation; death domain; MORT MODULE; ICE-like family protease; kinase; TRAF domain; inflammation; cell death; tumour; HIV; infection.	
OS	XX	Homo sapiens.	
XX	PN	WO9841624-A1.	
XX	PD	24-SEP-1998.	
XX	PF	19-MAR-1999; 98WO-IL000125.	
XX	PR	19-MAR-1997; 97IL-00120485.	
XX	PA	(YEDA) YEDA RES & DEV CO LTD.	
XX	PI	Wallach D, Kovalenko A;	
XX	PI	WPI: 1998-531565/45.	
DR	DR	N-PSDB; AAV57200.	
XX	PT	DATA encoding RIP-associated protein (RAP) - useful for, e.g. treatment of tumour cells or HIV-infected cells.	
PS	PS	Claim 10; Fig 2; 65pp; English.	
XX	CC	This sequence represent part of a human RIP-associated protein (RAP). The coding sequence was isolated from a B-cell library by a yeast 2-hybrid screen using the RIP protein devoid of its "death domain" as a bait. The screen isolated a clone of about 1.9 kb. Primers were generated based on the sequence and used to PCR amplify probes for screening a colon and heart cDNA library. A further 300 bp of sequence was determined, which was added to the 1.9 kb of sequence from the B-cell library. The encoded protein does not contain a "death domain", MORT MODULE, ICE-like family protease domain, kinase domain, nor TRAF domains. RAP was shown to bind only to RIP and not to TRADD, MORT-1, p55-R, p75-R or MACH. The protein can be used to modulate or mediate RIP modulated/mediated intracellular effects on the inflammation, cell death or cell survival pathways in which RIP is involved, e.g. for treating tumour cells or HIV-infected cells	
XX	XX	Sequence 591 AA;	
Query Match 91.1%; Score 2510; DB 2; Length 591;			
Best Local Similarity 99.6%; Pred. No. 2.2e-217;			
Matches 479; Conservative 0; Mismatches 0; Indels 2; Gaps 1;			
Qy	42	SNTRFTITLNYKDLTGDETLASGYVSGDLICILQDDIPAPNIPSTDSEHSLQNN	101
Db	113	SNTRFTITLNYKDLTGDETLASGYVSGDLICILQDDIPAPNIPSTDSEHSLQNN	172
Qy	102	EQPSLATSSNOTSMODEQPSDSFQGAAGSGVWVNDSDMLGPSQNFASFIQDNAHMAECT	161

Db	173	EQ--LATSSNOTSMODEQPSDSFQGAAGSGVWVNDSDMLGPSQNFASFIQDNAHMAECT	230
Qy	162	GFYPSEPMLCSESVEGQVPHSLETLYQSADCSANDALIVLHLLMLESGYIPQGTAKA	221
Db	231	GFYPSEPMLCSESVEGQVPHSLETLYQSADCSANDALIVLHLLMLESGYIPQGTAKA	290
Qy	222	LSMPEKWKLSGVYKLYQYWHPICEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP	281
Db	291	LSMPEKWKLSGVYKLYQYWHPICEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP	350
Qy	282	ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTRAQALNLPDVFGLVVLPLEKL	341
Db	351	ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTRAQALNLPDVFGLVVLPLEKL	410
Qy	342	RIFRLLDVRSVLISAVCRDLFTASNDPLLRFLYLDRFRDNTVRVQTDWKELYRKHHI	401
Db	411	RIFRLLDVRSVLISAVCRDLFTASNDPLLRFLYLDRFRDNTVRVQTDWKELYRKHHI	470
Qy	402	QRKESPKGRFVMLLPSSSTHTTIPFVNPPLHPPSPSSRLPPGIIIGGEYDQRTPLPVGDDPI	461
Db	471	QRKESPKGRFVMLLPSSSTHTTIPFVNPPLHPPSPSSRLPPGIIIGGEYDQRTPLPVGDDPI	530
Qy	462	SSLIPGCGTSPQFPPLPRFPDPVGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSF	521
Db	531	SSLIPGCGTSPQFPPLPRFPDPVGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSF	590
Qy	522	M 522	
Db	591	M 591	
RESULT 8			
AAW83047	AAW83047 standard; protein; 482 AA.		
XX	AC	AAW83047;	
XX	DT	16-AUG-2000 (first entry)	
XX	DE	F-box protein FBP-7.	
XX	XX	F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist; proliferative disorder; differentiative disorder; breast cancer; prostate cancer; ovarian cancer; cancer; small cell lung carcinoma; immune disorder; cardiovascular disorder; inflammatory disorder; human.	
OS	XX	Homo sapiens.	
XX	PN	WO200012679-A1.	
XX	PD	09-MAR-2000.	
XX	PF	27-AUG-1999; 99WO-US019560.	
XX	PR	28-AUG-1998; 98US-0098355P.	
XX	PR	03-FEB-1999; 99US-0118568P.	
XX	PR	15-MAR-1999; 99US-0124449P.	
XX	PA	(UANY) UNIV NEW YORK STATE.	
XX	PI	Chiaur DS, Pagano M, Latres E;	
XX	DR	WPI: 2000-256635/22.	
XX	DR	N-PSDB; AAZ93356.	
XX	PT	Novel nucleic acid for screening compounds useful for treating proliferative and differentiative disorders such as cancer and immune disorders comprises sequences encoding ubiquitin ligases.	
XX	PS	Claim 10; Fig 10a; 245pp; English.	
XX	CC	Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases	

Db 482 M 482

RESULT 10

AAU32109

ID AAU32109 standard; protein., 607 AA.

XX AC AAU32109;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #2600.

XX KW Human; vaccination; gene therapy; nutritional supplement;

XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US008656.

XX PR 18-APR-2000; 2000US-00552929.

XX PR 26-JAN-2001; 2001US-00770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic

XX PS vaccination, testing and therapy.

XX PS Claim 20; Page 556; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The

XX CC polypeptides and antibodies to the polypeptides are useful for

XX CC determining the presence of or predisposition to a disease associated

XX CC with altered levels of polypeptide. The polypeptides are also useful for

XX CC identifying agents (agonists and antagonists) that bind to them. Cells

XX CC expressing the proteins are useful for identifying a therapeutic agent

XX CC for use in treatment of a pathology related to aberrant expression or

XX CC physiological interactions of the polypeptide. Vectors comprising the

XX CC nucleic acids encoding the polypeptides and cells genetically engineered

XX CC to express them are also useful for producing the proteins. The proteins

XX CC are useful in genetic vaccination, testing and therapy, and can be used

XX CC as nutritional supplements. They may be used to increase stem cell

XX CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon

XX CC and/or nerve tissue growth or regeneration; immune suppression and/or

XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

XX CC AAU29510-AAU3304 represent the amino acid sequences of novel human

XX CC secreted proteins of the invention

XX SQ Sequence 607 AA;

Query Match 88.9%; Score 2448.5; DB 4; Length 607;

Best Local Similarity 90.8%; Pred. No. 8.3e-212;

Matches 481; Conservative 7; Mismatches 33; Indels 9; Gaps 5;

QY 1 MRLRVLKRTWPLEVPEPETEPTLGLHRLSHLSLLCTWGYSSNTFTITLNYKDLTGDE 60

DB 36 MRLRVLKRTWPLEVPEPETEPTLGLHRLSHLSLLCTWGYSSNTFTITLNYKDLTGDE 95

QY 61 ETLASYGVISGDLICILQDDIPAPNIPSSITDSEHSSIQNNQPSLATSSNQTSMQDQOP 120

DB 96 ETLASYGVISGDLICILQDDIPAPNIPSSITDSEHSSIQNNQPSLATSSNQTSMQDQOP 155

QY 121 SDSFOGQAQSGVWDDSLMGPSONFEAESIQDNAHMAEGTGFPSEPMLCSESVEGQVP 180

Db 156 SDSFOGQAQSGVWDDSLMGPSONFEAESIQDNAHMAEGTGFPSEPMLCSESVEGQVP 215

QY 181 HSLETLYOSADCSANDALIVLIHLLMLESYIPOGTEAKALSMPEKWKLSGVYKLYMH 240

Db 216 HSLETLYOSADCSANDALIVLIHLLMLESYIPOGTEAKALSMPEKWKLSGVYKLYMH 275

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300

Db 276 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 335

QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVLPLELKLRIFFRLLDVRSVLSAVCR 360

Db 336 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVLPLELKLRIFFRLLDVRSVLSAVCR 395

QY 361 DLFTASNDPLLRWRLYLRFDRDNTVRVQDQTKELYRKHRIQRKESPKGRFVMLLPSSSTH 420

Db 396 DLFTASNDPLLRWRLYLRFDRDNTVRVQDQTKELYRKHRIQRKESPKGRFVMLLPSSSTH 455

QY 421 TIFYPNPLHPRPFPSSRLPGIIGGEYDQRP-TLPYVVGDPISLIPGP-GETPS-QFPP 477

Db 456 TIFYPNPLHPRPFPSSRLPGIIGGEYDQRP-TLPYVVGDPISLIPGP-GETPS-QFPP 515

QY 478 -----LRPRFDPVGLPGNPLPGRGGNDPFPFRSRRGPTDGRLSFM 522

Db 516 TETHALNPSPFISGRDNPQSCPGAEGGPNRTRFPLRPOP-GGRANLM 564

RESULT 11

ABB90109

ID ABB90109 standard; protein; 462 AA.

XX AC ABB90109;

XX DT 24-MAY-2002 (first entry)

XX DE Human polypeptide SEQ ID NO 2485.

XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

XX KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;

XX KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;

XX KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;

XX KW neurological disease; infection; human; secreted protein.

XX OS Homo sapiens.

XX PN WO200190304-A2.

XX PD 29-NOV-2001.

XX PF 18-MAY-2001; 2001WO-US016450.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birse CE, Rosen CA;

XX DR WPI; 2002-122018/16.

XX DR N-PSDB; ABL90518.

XX PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and

XX PT prevention of neural, immune system, muscular, reproductive,

XX PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative

XX PT disorders.

XX PS Claim 11; SEQ ID NO 2485; 2081pp + Sequence Listing; English.

XX CC The invention relates to novel genes (ABL89449-ABL90853) and proteins

XX CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating

XX CC medical conditions e.g. by protein or gene therapy. The genes are

XX CC isolated from a range of human tissues disclosed in the specification.

XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 5; Length 462;
Best Local Similarity 88.1%; Pred. No. 5,8e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
QY 1 MRLRVLLKRTWPLEVPETETPLGHLRSHLRSLCTWGYSSNTFTITLNYKDPDTGDE 60
DB 1 MRLRVLLKRTWPLEVPETETPLGHLRSHLRSLCTWGYSSNTFTITLNYKDPDTGDE 60
QY 61 ETLASGVISGDLICLILODDIPAPNIPSSDTSEHSSLQNNQPSLATSSNOTSQDDEP 120
DB 61 ETLASGVISGDLICLILODDIPAPNIPSSDTSEHSSLQNNQPSLATSSNOTSQDDEP 120
QY 121 SDSFOGQAQSGVNDSDMLGSPQNFPEABSIQDNAMHAEAGTGFPSEPMCLSESVEGQVP 180
DB 121 SDSFOGQAQSGVNDSDMLGSPQNFPEABSIQDNAMHAEAGTGFPSEPMCLSESVEGQVP 180
QY 181 HSLETLYSADCSNDALIVLHLMLESYVPOGTEAKALSMPEKWLKGVYKLYQYMH 240
DB 181 HSLETLYSADCSNDALIVLHLMLESYVPOGTEAKALSMPEKWLKGVYKLYQYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKQLQLLPESFICKELGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVN----- 262
QY 301 LQKLSRLFKDQLVYPLLAFTROALNPDVFLWLPLEKLIFRLLDVRSLVSACVR 360
DB 263 -----ALNLPDVFLWLPLEKLIFRLLDVRSLVSACVR 300
QY 361 DLFTASNDPLLRFLYLRDRDNTVRVQDTWKELYRKHIOKESPKGRFVMLLPSSHT 420
DB 301 DLFTASNDPLLRFLYLRDRDNTVRVQDTWKELYRKHIOKESPKGRFVMLLPSSHT 360
QY 421 TIFPYNPLHPPFPSSRLPPGIIGGEVDORTLPIYVGDPISSLIPGGETPSQFPPLRP 480
DB 361 TIFPYNPLHPPFPSSRLPPGIIGGEVDORTLPIYVGDPISSLIPGGETPSQFPPLRP 420
QY 481 RPDVPGLPGNPILPGRGGPNDRPFRPSRCRPTDGRLSFM 522
DB 421 RPDVPGLPGNPILPGRGGPNDRPFRPSRCRPTDGRLSFM 462

RESULT 12
ID ADAS7586
ID ADAS7586 standard; protein; 462 AA.
XX ADAS7586;
AC ADAS7586;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human secreted protein #566.
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;

KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX Homo sapiens.
OS WO2002102994-A2.
PN 27-DEC-2002.
PD 19-MAR-2002; 2002WO-US008278.
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
PI WPI; 2003-167512/16.
XX N-PSDB; ADA56693.
XX New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX Claim 13; SEQ ID NO 1779; 1754pp; English.
XX The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy) cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 6; Length 462;
Best Local Similarity 88.1%; Pred. No. 5,8e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
QY 1 MRLRVLLKRTWPLEVPETETPLGHLRSHLRSLCTWGYSSNTFTITLNYKDPDTGDE 60
DB 1 MRLRVLLKRTWPLEVPETETPLGHLRSHLRSLCTWGYSSNTFTITLNYKDPDTGDE 60
QY 61 ETLASGVISGDLICLILODDIPAPNIPSSDTSEHSSLQNNQPSLATSSNOTSQDDEP 120
DB 61 ETLASGVISGDLICLILODDIPAPNIPSSDTSEHSSLQNNQPSLATSSNOTSQDDEP 120

QY 121 SDSFGQAAQSGVWDDSMGLGSPQNFSESIQDNAMHAEAGTGFPSEPMCLSESVEGQVP 180
DB |||||
QY 121 SDSFGQAAQSGVWDDSMGLGSPQNFSESIQDNAMHAEAGTGFPSEPMCLSESVEGQVP 180
DB |||||
QY 181 HSLETLQYQADCSNDALIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVYKLYQYMH 240
DB |||||
QY 181 HSLETLQYQADCSNDALIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVYKLYQYMH 240
DB |||||
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
DB |||||
QY 241 PLCEGSSATLTCVPLGNLIVVN----- 262
QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLEKLRIFFLLDVRVSLSAVCR 360
DB |||||
QY 361 DLFTASNDPLLWRFLYLDRFRONTVRVQDQTKWELRYKRHHIQRKESPKGRFVMLLPSSSTH 420
DB |||||
QY 301 DLFTASNDPLLWRFLYLDRFRONTVRVQDQTKWELRYKRHHIQRKESPKGRFVMLLPSSSTH 360
DB |||||
QY 421 TIPFVFNPLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP 480
DB |||||
QY 361 TIPFVFNPLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP 420
DB |||||
QY 481 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
DB |||||
QY 421 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 462
DB |||||

RESULT 13
ADA41482
ID ADA41482 standard; protein; 462 AA.
XX
AC ADA41482;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnary; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
XX WPI; 2003-175238/17.
XX
XX New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 1; SEQ ID NO 1865; 3205pp; English.
XX
XX The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC

CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), infectious diseases (bacterial,
CC e.g. atherosclerosis, myocarditis), cardiovascular disorders (e.g.
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 6; Length 462;
Best Local Similarity 88.1%; Pred. No. 5.8e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
QY 1 MRLRVLLKRTWPTEPTETLGHLSRLSLCTGWGSSNTFTTLYNKDPLTGDE 60
DB |||||
QY 1 MRLRVLLKRTWPTEPTETLGHLSRLSLCTGWGSSNTFTTLYNKDPLTGDE 60
DB |||||
QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSLQNNQPSLATSSNOTSMQDEOP 120
DB |||||
QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSLQNNQPSLATSSNOTSMQDEOP 120
DB |||||
QY 121 SDSFGQAAQSGVWDDSMGLGSPQNFSESIQDNAMHAEAGTGFPSEPMCLSESVEGQVP 180
DB |||||
QY 121 SDSFGQAAQSGVWDDSMGLGSPQNFSESIQDNAMHAEAGTGFPSEPMCLSESVEGQVP 180
DB |||||
QY 181 HSLETLQYQADCSNDALIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVYKLYQYMH 240
DB |||||
QY 181 HSLETLQYQADCSNDALIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVYKLYQYMH 240
DB |||||
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
DB |||||
QY 241 PLCEGSSATLTCVPLGNLIVVN----- 262
QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLEKLRIFFLLDVRVSLSAVCR 360
DB |||||
QY 361 DLFTASNDPLLWRFLYLDRFRONTVRVQDQTKWELRYKRHHIQRKESPKGRFVMLLPSSSTH 420
DB |||||
QY 301 DLFTASNDPLLWRFLYLDRFRONTVRVQDQTKWELRYKRHHIQRKESPKGRFVMLLPSSSTH 360
DB |||||
QY 421 TIPFVFNPLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP 480
DB |||||
QY 361 TIPFVFNPLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP 420
DB |||||
QY 481 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
DB |||||
QY 421 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 462
DB |||||
RESULT 14
ABR48139
ID ABR48139 standard; protein; 462 AA.

XX AC ABR48139;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human secreted protein, SEQ ID 1030.
 XX KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
 KW vulnerable; antiinflammatory; nootropic; neuroprotective;
 KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
 XX OS Homo sapiens.
 XX PN WO200295010-A2.
 XX PD 28-NOV-2002.
 XX PF 19-MAR-2002; 2002WO-US009785.
 XX PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX DR WPI; 2003-129429/12.
 XX PT Novel human secreted proteins, useful for detecting, preventing,
 PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
 PT disorders such as arrhythmia.
 XX PS Claim 13; SEQ ID NO 1030; 1881pp; English.
 XX CC The present invention relates to novel human secreted proteins (ABR47633-
 CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
 CC and their coding sequences are useful for the preparation of a diagnostic
 CC or pharmaceutical composition for diagnosing or treating a cardiovascular
 CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
 CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, renal disorders,
 CC proliferative disorders and/or cancerous diseases and conditions, for
 CC wound healing and epithelial cell proliferation, to treat inflammation or
 CC infection, for treating thrombosis and arteriosclerosis, for treating or
 CC preventing neural damage which occurs in neuronal disorders or
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 CC disease, to enhance bone and periodontal regeneration and aid in tissue
 CC transplants or bone grafts, to prevent skin aging or hair loss, to
 CC stimulate growth and differentiation of haematopoietic cells and bone
 CC marrow cells when used in combination with other cytokines, to maintain
 CC organs before transplantation or for supporting cell culture of primary
 CC tissues, to increase or decrease differentiation or proliferation of
 CC embryonic stem cells, or to modulate mammalian characteristics or
 CC metabolism. Note: The sequence data for this patent was published in
 CC electronic format and is available from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 462 AA;
 Query Match 87.3%; Score 2404; DB 6; Length 462;
 Best Local Similarity 88.1%; Pred. No. 5.8e-208;
 Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
 QY 1 MRLRLRLKRTWPLEVETETLGLHRLSHLSLLCTWGYSSNTRFTITLNYKDLTGDE 60
 DB 1 MRLRLRLKRTWPLEVETETLGLHRLSHLSLLCTWGYSSNTRFTITLNYKDLTGDE 60
 QY 61 ETLASYGVISGDLICLLIQDDIPAPNIPSSDTSDEHSSLLQNEQPSLATSSNOTSQDDEP 120
 DB 61 ETLASYGVISGDLICLLIQDDIPAPNIPSSDTSDEHSSLLQNEQPSLATSSNOTSQDDEP 120

QY 121 SDSFGQAAQSGVWDDSMQLPSONFEAEISTODNAHMAEGTGFYPSBPMLCSESVEGQVP 180
 DB 121 SDSFGQAAQSGVWDDSMQLPSONFEAEISTODNAHMAEGTGFYPSBPMLCSESVEGQVP 180
 QY 181 HSLETLVQSADCSANDALIVLIHLLMLESYVPOGTEAKALSMPEKWKLSGVYKLYQYMH 240
 DB 181 HSLETLVQSADCSANDALIVLIHLLMLESYVPOGTEAKALSMPEKWKLSGVYKLYQYMH 240
 QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKKJENGVANIYKD 300
 DB 241 PLCEGSSATLTCVPLGNLIVVN----- 262
 QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPVFGVLVVLPLELKLRIFRLLDVRSVLSAVCR 360
 DB 263 -----ALNLPDVFGVLVVLPLELKLRIFRLLDVRSVLSAVCR 300
 QY 361 DLFTASNDPLLRFLYLRDFRDNTVRVQDTPWKELYKRHIQRKESPKGRFVMLLPSSSTH 420
 DB 301 DLFTASNDPLLRFLYLRDFRDNTVRVQDTPWKELYKRHIQRKESPKGRFVMLLPSSSTH 360
 QY 421 TIFYPNPLHPRPFSSRLPGIIGGEYDQRTPLPYVGDPISLIPGGETPSQFPPLRP 480
 DB 361 TIFYPNPLHPRPFSSRLPGIIGGEYDQRTPLPYVGDPISLIPGGETPSQFPPLRP 420
 QY 481 RFDVGPLPGNPILPGRGGNDPFRPPSRGRPTDGRLSFM 522
 DB 421 RFDVGPLPGNPILPGRGGNDPFRPPSRGRPTDGRLSFM 462

RESULT 15
 ADC74596
 ID ADC74596 standard; protein; 462 AA.
 XX AC ADC74596;
 XX DT 01-JAN-2004 (first entry)
 XX DE Human secreted protein - SEQ ID 1229.
 KW antinaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
 KW antidiabetic; immunosuppressive; dermatological; nephrotropic;
 KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnary; cytostatic;
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
 KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
 KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
 KW human.
 XX OS Homo sapiens.
 XX PN WO2003038063-A2.
 XX PD 08-MAY-2003.
 XX PF 19-MAR-2002; 2002WO-US008277.
 XX PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX DR WPI; 2003-430516/40.
 DR N-PSDB; ADC73981.
 XX PT New human secreted polypeptide for diagnosing, preventing or treating
 PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
 PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
 PT atherosclerosis).

```
XX Claim 16; SEQ ID NO 1229; 2272pp; English.
XX
CC The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting
CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC The current sequence is that of the human secreted protein of the
CC invention.
XX
SQ Sequence 462 AA;
Query Match 87.3%; Score 2404; DB 7; Length 462;
Best Local Similarity 88.1%; Pred. No. 5.8e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
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Search completed: July 19, 2005, 20:16:54
Job time : 170 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2005, 20:19:59 ; Search time 161 Seconds
(without alignments)
1258.598 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLRVLRLKRTWPLEVPETE.....DRFPFRSGRPTDRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1736639 seqs, 3818149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA.*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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 - 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2754	100.0	522	9	US-09-927-458-2
2	2754	100.0	522	14	Sequence 2, Appli
3	2744	99.6	522	16	Sequence 10, Appl
4	2489	90.4	482	13	Sequence 14, Appl
5	2489	90.4	482	17	Sequence 14, Appl
6	2404	87.3	462	10	Sequence 200, App
7	2404	87.3	462	15	Sequence 2485, Ap
8	2404	87.3	462	15	Sequence 200, App
9	2404	87.3	497	10	Sequence 435, App
10	2404	87.3	497	10	Sequence 435, App
11	2270	82.4	443	16	Sequence 8, Appli

12	1527	55.4	317	15	US-10-264-237-2484	Sequence 2484, Ap
13	1238	45.0	231	16	US-10-408-765A-752	Sequence 752, App
14	1086	33.4	221	15	US-10-094-749-1723	Sequence 1723, Ap
15	714	25.9	174	10	US-09-397-945-434	Sequence 434, App
16	714	25.9	174	15	US-10-653-595-209	Sequence 209, App
17	714	25.9	174	15	US-10-653-595-434	Sequence 434, App
18	714	25.9	175	10	US-09-397-945-209	Sequence 209, App
19	396	14.4	76	14	US-10-029-386-27908	Sequence 27908, A
20	249	9.0	47	14	US-10-029-386-33496	Sequence 33496, A
21	215.5	7.8	500	16	US-10-739-930-9910	Sequence 9910, A
22	211	7.7	485	15	US-10-425-114-59110	Sequence 59110, A
23	207	7.5	485	15	US-10-425-114-59111	Sequence 59111, A
24	201	7.3	485	15	US-10-425-114-60984	Sequence 60984, A
25	198	7.0	447	16	US-10-425-115-349540	Sequence 349540,
26	194	7.0	39	13	US-10-042-417-21	Sequence 21, Appl
27	194	7.0	39	17	US-10-652-928-21	Sequence 21, Appl
28	189	6.9	38	11	US-09-801-348-47	Sequence 47, Appl
29	164	6.0	38	11	US-09-801-348-49	Sequence 49, Appl
30	144	5.2	408	15	US-10-264-237-1835	Sequence 1835, Ap
31	142	5.2	1131	16	US-10-425-115-355048	Sequence 355048,
32	140	5.1	379	15	US-10-264-049-2807	Sequence 2807, Ap
33	139	5.0	327	13	US-10-042-417-58	Sequence 58, Appl
34	139	5.0	327	16	US-10-679-246-12	Sequence 12, Appl
35	139	5.0	327	17	US-10-652-928-58	Sequence 58, Appl
36	137	5.0	664	16	US-10-437-963-176808	Sequence 176808,
37	129.5	4.7	197	16	US-10-425-115-356769	Sequence 356769,
38	128.5	4.7	842	17	US-10-732-923-13573	Sequence 13573, A
39	128.5	4.7	850	17	US-10-732-923-13572	Sequence 13572, A
40	126	4.6	344	14	US-10-061-043A-27	Sequence 27, Appl
41	126	4.6	344	15	US-10-060-634C-27	Sequence 27, Appl
42	126	4.6	355	14	US-10-061-043A-35	Sequence 35, Appl
43	126	4.6	355	15	US-10-060-634C-35	Sequence 35, Appl
44	126	4.6	355	15	US-10-094-749-2883	Sequence 2883, Ap
45	125.5	4.6	754	16	US-10-437-963-134895	Sequence 134895,

ALIGNMENTS

RESULT 1
US-09-927-458-2
; Sequence 2, Application US/09927458
; Patent No. US20020036024A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR F
; TITLE OF INVENTION: AND OTHER PROTEINS
; FILE REFERENCE: WALLACH-22A
; CURRENT APPLICATION NUMBER: US/09/927,458
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/IL98/00125
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: IL 120485
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: 09/381,358
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-927-458-2

Query Match 100.0%; Score 2754; DB 9; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.4e-223;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 2, Application US/10245593			
; Publication No. US2003039646A1			
; GENERAL INFORMATION:			
; APPLICANT: WALLACH, David			
; APPLICANT: KOVALENKO, Andrei			
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR F			
; FILE REFERENCE: WALLACH=22A			
; CURRENT APPLICATION NUMBER: US/10/245,593			
; PRIOR FILING DATE: 2002-09-18			
; PRIOR APPLICATION NUMBER: US/09/927,458			
; PRIOR FILING DATE: 2001-08-13			
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; PRIOR FILING DATE: 1998-03-19			
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; PRIOR APPLICATION NUMBER: 09/381,358			
; PRIOR FILING DATE: 1999-09-20			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 2			
; LENGTH: 522			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
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RESULT 3			
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; Sequence 10, Application US/10679246			
; Publication No. US20040163138A1			
; GENERAL INFORMATION:			
; APPLICANT: Reed, John C.			
; APPLICANT: Matsuzawa, Shu-ichi			
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved			
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto			
; FILE REFERENCE: 66821-235			
; CURRENT APPLICATION NUMBER: US/10/679,246			
; CURRENT FILING DATE: 2003-10-02			
; PRIOR APPLICATION NUMBER: US 09/591,694			
; PRIOR FILING DATE: 2000-06-09			
; NUMBER OF SEQ ID NOS: 50			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 10			
; LENGTH: 522			
; TYPE: PRT			
; ORGANISM: Homo sapien			
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; Sequence 14, Application US/10042417
; Publication No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-5
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-417-14

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Best Local Similarity 98.1%; Pred. No. 5.1e-201;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy 162 GYPSEPMCLCSSEVQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 221
Db 122 GYPSEPLLCSSVQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 181
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Db 122 GYPSEPLLCSSVQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 181
Qy 282 ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVPLLEKL 341
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Qy 342 RIFRLDVRSVLSAVCRDLFTASNDPLLRFLYLRDFRNTVRVQTDWKELYRKHHI 401
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Db 302 RIFRLDVRSVLSAVCRDLFTASNDPLLRFLYLRDFRNTVRVQTDWKELYRKHHI 361
Qy 462 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPPFPSSRLPPGIIGEYDQRTPLPVGDP 521
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Qy 482 SSLIFPGGETSQFPPLRPFRFDPVGLPGNPILPGRGPNDRFPFRSGRPTDGRLSF 521

Db 422 SSLIFPGGETSQFPPLRPFRFDPVGLPGNPILPGRGPNDRFPFRSGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482

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US-10-652-928-14
; Sequence 14, Application US/10652928
; Publication No. US20050079558A1
; GENERAL INFORMATION:
; APPLICANT: Chaiur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/652,928
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US/09/385,219A
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-928-14

Query Match 90.4%; Score 2489; DB 17; Length 482;
Best Local Similarity 98.1%; Pred. No. 5.1e-201;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 42 SNTRFTITLNYKDPITGDETLASVIGSGDLICILIODDIPAPNIPSTDSEHSSLQNN 101
Db 2 SNTRFTITLNYKDPITGDETLASVIGSGDLICILIODDIPAPNIPSTDSEHSSLQNN 61
Qy 102 EOPSLATSSNOTSMODEPDSFQQAQSGVWVNDSDMLGPSONFEAESIQDNAHMAEGT 161
Db 62 EOPSLATSSNOTSIQDEQPSDSFQQAQSGVWVNDSDMLGPSONFEAESIQDNAHMAEGT 121
Qy 162 GYPSEPMCLCSSEVQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 221
Db 122 GYPSEPLLCSSVQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 181
Qy 222 LSMPEKWLKSGVYKQYMHPLCEGSSATLTCVPLGNLIWVATLKNINNEIRSVKRLQLLP 281
Db 122 GYPSEPLLCSSVQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 181
Qy 282 ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVPLLEKL 341
Db 242 ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVPLLEKL 301
Qy 342 RIFRLDVRSVLSAVCRDLFTASNDPLLRFLYLRDFRNTVRVQTDWKELYRKHHI 401
Db 302 RIFRLDVRSVLSAVCRDLFTASNDPLLRFLYLRDFRNTVRVQTDWKELYRKHHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPPFPSSRLPPGIIGEYDQRTPLPVGDP 461
Db 362 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPPFPSSRLPPGIIGEYDQRTPLPVGDP 421
Qy 462 SSLIFPGGETSQFPPLRPFRFDPVGLPGNPILPGRGPNDRFPFRSGRPTDGRLSF 521
Db 422 SSLIFPGGETSQFPPLRPFRFDPVGLPGNPILPGRGPNDRFPFRSGRPTDGRLSF 481
Qy 522 M 522

QY 361 DLFTASNDPLLRFLYLRDPRDNTVRVQDTHKELYRKHIOKESPKGRFVMLLPSSSTH 420
DB 301 DLFTASNDPLLRFLYLRDPRDNTVRVQDTHKELYRKHIOKESPKGRFVMLLPSSSTH 360
QY 421 TIPFPNPLHPRPPSSRLPGIIGGEYDQRTPLPVGDPISSLLPGGETPSQFPPLRP 480
DB 361 TIPFPNPLHPRPPSSRLPGIIGGEYDQRTPLPVGDPISSLLPGGETPSQFPPLRP 420
QY 481 RFDVGPPLGPNPILPGRGGPNDRPFRPSRGRPTDGRLSFM 522
DB 421 RFDVGPPLGPNPILPGRGGPNDRPFRPSRGRPTDGRLSFM 462

RESULT 8

US-10-653-595-200
; Sequence 200, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.

; TITLE OF INVENTION: 95 Human secreted proteins

; FILE REFERENCE: PZ027P1C1

; CURRENT APPLICATION NUMBER: US/10/653,595

; CURRENT FILING DATE: 2003-09-03

; PRIOR APPLICATION NUMBER: US 09/397945

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: PCT/US99/05804

; PRIOR FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: 60/078,566

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,576

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,573

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,574

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,579

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/080,314

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/080,312

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/078,578

; PRIOR FILING DATE: 1998-03-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 470

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 200

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (115)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-653-595-200

Query Match 87.3%; Score 2404; DB 15; Length 462;

Best Local Similarity 88.1%; Pred. No. 7, 1e-194;

Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLVPEPTPLGLHRLSHRLSLICTWGYSSNTRFTITLNYKDLTGDE 60

DB 1 MRLRVLLKRTWPLVPEPTPLGLHRLSHRLSLICTWGYSSNTRFTITLNYKDLTGDE 60

QY 61 ETLASVGVSGDLICLLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNOTSMODEQP 120

DB 61 ETLASVGVSGDLICLLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNOTSMODEQP 120

QY 121 SDSFGQAAQAGVWDDSMGLPQNFQESIQDNHMAEGTGYFSEPMLCSEVGGQVP 180

DB 121 SDSFGQAAQAGVWDDSMGLPQNFQESIQDNHMAEGTGYFSEPMLCSEVGGQVP 180

QY 181 HSLETLYOSADCSANDALIVLIHLLMLESYIPOGTEAKALSMPEKWKLSGVYKLOYNH 240
DB 181 HSLETLYOSADCSANDALIVLIHLLMLESYIPOGTEAKALSMPEKWKLSGVYKLOYNH 240
QY 241 PLCGSSATLTCVPLGNLIVVNATLKKINNEIRSVKRLQLLPESFTCKEKLGENVANIYKD 300
DB 241 PLCGSSATLTCVPLGNLIVN----- 262
QY 301 LQKLSRLFKDQOLVPLLAFTQALNLPDVFGVLVLPLELKLIIFRLLDVRSVLSAVCR 360
DB 263 -----ALNLPDVFGVLVLPLELKLIIFRLLDVRSVLSAVCR 300
QY 361 DLFTASNDPLLRFLYLRDPRDNTVRVQDTHKELYRKHIOKESPKGRFVMLLPSSSTH 420
DB 301 DLFTASNDPLLRFLYLRDPRDNTVRVQDTHKELYRKHIOKESPKGRFVMLLPSSSTH 360
QY 421 TIPFPNPLHPRPPSSRLPGIIGGEYDQRTPLPVGDPISSLLPGGETPSQFPPLRP 480
DB 361 TIPFPNPLHPRPPSSRLPGIIGGEYDQRTPLPVGDPISSLLPGGETPSQFPPLRP 420
QY 481 RFDVGPPLGPNPILPGRGGPNDRPFRPSRGRPTDGRLSFM 522
DB 421 RFDVGPPLGPNPILPGRGGPNDRPFRPSRGRPTDGRLSFM 462

RESULT 9

US-09-397-945-435
; Sequence 435, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: 95 Human secreted proteins

; FILE REFERENCE: PZ027P1

; CURRENT APPLICATION NUMBER: US/09/397,945

; CURRENT FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: PCT/US99/05804

; PRIOR FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: 60/078,566

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,576

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,573

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,574

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,579

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/080,314

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/080,312

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/078,578

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,581

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,577

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,563

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/080,313

; PRIOR FILING DATE: 1998-04-01

; NUMBER OF SEQ ID NOS: 470

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 435

; LENGTH: 497

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (150)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-397-945-435

Query Match 87.3%; Score 2404; DB 10; Length 497;
Best Local Similarity 88.1%; Pred. No. 7.9e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPEPETGLHLRSHLRSLLLCTWGYSSNTRFTTILNYKDLPTGDE 60
DB 36 MRLRVLLKRTWPLEVPEPETGLHLRSHLRSLLLCTWGYSSNTRFTTILNYKDLPTGDE 95
QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSIQNNEQPSLATSSNOTSQDQOP 120
DB 96 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSIQNNEQPSLATSSNOTSQDQOP 155
QY 121 SDSFOGQAQSGVWVNDSDMLGFSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
DB 156 SDSFOGQAQSGVWVNDSDMLGFSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 215
QY 181 HSLETLYOSADCSANDALIVLIHLLMESGYIPOGTEAKALSMPEKWKLSGVYKLOYMH 240
DB 216 HSLETLYOSADCSANDALIVLIHLLMESGYIPOGTEAKALSMPEKWKLSGVYKLOYMH 275
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
DB 276 PLCEGSSATLTCVPLGNLIVN----- 297
QY 301 LQKLSRLFKDQLVVYPLLAFTROALNLPDVFGVLVLPLELKLRIIFRLLDVRSVLSLSAVCR 360
DB 298 -----ALNLPDVFGVLVLPLELKLRIIFRLLDVRSVLSLSAVCR 335
QY 361 DLFTASNDPLLWRFLYLRDFRONTVRVQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
DB 336 DLFTASNDPLLWRFLYLRDFRONTVRVQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 395
QY 421 TIPFYPNPLHPRPFPSSRLPGIIGGEYDQRTPLPYVGDPISSLIIPGCGETPSQFPPLRP 480
DB 396 TIPFYPNPLHPRPFPSSRLPGIIGGEYDQRTPLPYVGDPISSLIIPGCGETPSQFPPLRP 455
QY 481 RFDVPGPLPGPNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 522
DB 456 RFDVPGPLPGPNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 497

RESULT 10
US-10-653-595-435
; Sequence 435, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027PIC1
; CURRENT APPLICATION NUMBER: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 435
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (150)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-435

Query Match 87.3%; Score 2404; DB 15; Length 497;
Best Local Similarity 88.1%; Pred. No. 7.9e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPEPETGLHLRSHLRSLLLCTWGYSSNTRFTTILNYKDLPTGDE 60
DB 36 MRLRVLLKRTWPLEVPEPETGLHLRSHLRSLLLCTWGYSSNTRFTTILNYKDLPTGDE 95
QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSIQNNEQPSLATSSNOTSQDQOP 120
DB 96 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSIQNNEQPSLATSSNOTSQDQOP 155
QY 121 SDSFOGQAQSGVWVNDSDMLGFSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
DB 156 SDSFOGQAQSGVWVNDSDMLGFSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 215
QY 181 HSLETLYOSADCSANDALIVLIHLLMESGYIPOGTEAKALSMPEKWKLSGVYKLOYMH 240
DB 216 HSLETLYOSADCSANDALIVLIHLLMESGYIPOGTEAKALSMPEKWKLSGVYKLOYMH 275
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
DB 276 PLCEGSSATLTCVPLGNLIVN----- 297
QY 301 LQKLSRLFKDQLVVYPLLAFTROALNLPDVFGVLVLPLELKLRIIFRLLDVRSVLSLSAVCR 360
DB 298 -----ALNLPDVFGVLVLPLELKLRIIFRLLDVRSVLSLSAVCR 335
QY 361 DLFTASNDPLLWRFLYLRDFRONTVRVQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
DB 336 DLFTASNDPLLWRFLYLRDFRONTVRVQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 395
QY 421 TIPFYPNPLHPRPFPSSRLPGIIGGEYDQRTPLPYVGDPISSLIIPGCGETPSQFPPLRP 480
DB 396 TIPFYPNPLHPRPFPSSRLPGIIGGEYDQRTPLPYVGDPISSLIIPGCGETPSQFPPLRP 455
QY 481 RFDVPGPLPGPNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 522
DB 456 RFDVPGPLPGPNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 497

RESULT 11
US-10-679-246-8
; Sequence 8, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: in Protein Degradation, Products and Methods Related Thereo
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-8

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Query Match      82.4%; Score 2270; DB 16; Length 443;
Best Local Similarity 99.8%; Pred. No. 1.4e-182;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 92 DSEHSSLNQNEOPSLSATSSNQTSMODEQSDSFQGAQSGVWDDSMLGPSQNFSEESI 151
DB 13 DSEHSSLNQNEOPSLSATSSNQTSMODEQSDSFQGAQSGVWDDSMLGPSQNFSEESI 72
QY 152 QDNAHMAEGTGYFSEPMLECSSEVSGQVPHSLSTLYQSADCSANDALIVLHLLMLESG 211
DB 73 QDNAHMAEGTGYFSEPMLECSSEVSGQVPHSLSTLYQSADCSANDALIVLHLLMLESG 132
QY 212 YIPOGTEAKALSMPEKWKLSGVYKLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEI 271
DB 133 YIPOGTEAKALSMPEKWKLSGVYKLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEI 192
QY 272 RVKRLQLLPEGFCICEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFG 331
DB 193 RVKRLQLLPEGFCICEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFG 252
QY 332 LVVLPLELKLRIFRLLDVRSLSSAVCRDLFTASNDPPLLWRFLYLDRFRONTVRVQD 391
DB 253 LVVLPLELKLRIFRLLDVRSLSSAVCRDLFTASNDPPLLWRFLYLDRFRONTVRVQD 312
QY 392 WKELYRKHHIQKESPKGRFVMLPSSTHTIPFPNPLHPRPPSSRLPPGIIGGEYDQR 451
DB 313 WKELYRKHHIQKESPKGRFVMLPSSTHTIPFPNPLHPRPPSSRLPPGIIGGEYDQR 372
QY 452 PTLVYVGPDISSLIIPGGETPSQFPPLRPRDPVGLPGPNLPILGRGPNDRFPFRSR 511
DB 373 PTLVYVGPDISSLIIPGGETPSQFPPLRPRDPVGLPGPNLPILGRGPNDRFPFRSR 432
QY 512 GRPTDGRLSFM 522
DB 433 GRPTDGRLSFM 443

RESULT 12
US-10-264-237-2484
; Sequence 2484, Application US/10264237
; Publication No. US2004000941A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAI31P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2484
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2484

Query Match      55.4%; Score 1527; DB 15; Length 317;
Best Local Similarity 94.0%; Pred. No. 4.3e-120;
Matches 300; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

QY 115 MODEQPSDSFQGAQSGVWDDSMLGPSQNFSEESIQDNAHMAEGTGYFSEPMLECS 174
DB 1 MODEQPSDSFQGAQSGVWDDSMLGPSQNFSEESIQDNAHMAEGTGYFSEPMLECS 60
QY 175 VEGQVPHSLSTLYQSADCSANDALIVLHLLMLESGYIPQGTAKALSMPEKWKLSGVY 234
DB 61 VEGQVPHSLSTLYQSADCSANDALIVLHLLMLESGYIPQGTAKALSMPEKWKLSGVY 120
QY 235 KLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPSFICKEKLGENV 294
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DB 121 KLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPSFICKEKLGENV 180
QY 295 ANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLPLELKLRIFRLLDVRSL 354
DB 181 ANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLPLELKLRIFRLLDVRSL 240
QY 355 LSACVCRDLFTASNDPPLLWRFLYLDRFRONTVRVQDQDWKELYRKHHIQKESPKGRF -V 412
DB 241 LSACVCRDLFTASNDPPLLWRFLYLDRFRONTVRVQDQDWKELYRKHHIQKESPKGRVCDA 300
QY 413 MLLPSSSTHTIPFPNPLHP 431
DB 301 PAIVNSHHSI--LSQPLAP 317

RESULT 13
US-10-408-765A-752
; Sequence 752, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 752
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-752

Query Match      45.0%; Score 1238; DB 16; Length 231;
Best Local Similarity 100.0%; Pred. No. 6.7e-96;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 ENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLPLELKLRIFRLLDVR 351
DB 1 ENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLPLELKLRIFRLLDVR 60
QY 352 VLSLSAVCRDLFTASNDPPLLWRFLYLDRFRONTVRVQDQDWKELYRKHHIQKESPKGRF 411
DB 61 VLSLSAVCRDLFTASNDPPLLWRFLYLDRFRONTVRVQDQDWKELYRKHHIQKESPKGRF 120
QY 412 VMLPSSSTHTIPFPNPLHPRPPSSRLPPGIIGGEYQORPTLPVGDPISSLIIPGGET 471
DB 121 VMLPSSSTHTIPFPNPLHPRPPSSRLPPGIIGGEYQORPTLPVGDPISSLIIPGGET 180
QY 472 PSQPPPLRPRDPVGLPGPNLPILGRGPNDRFPFRSRGRTDGRLSFM 522
DB 181 PSQPPPLRPRDPVGLPGPNLPILGRGPNDRFPFRSRGRTDGRLSFM 231

RESULT 14
US-10-094-749-1723
; Sequence 1723, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
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OM protein - protein search, using sw model

Run on: July 19, 2005, 20:13:18 ; Search time 25 Seconds
(without alignments)
1558.672 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLRVLKRTWPLEVPETE.....DRFPFRSGRPTDGLRSLFM 522

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2748	99.8	557	4	US-09-949-016-10867
2	2744	99.6	522	4	US-09-591-694-10
3	2489	90.4	482	4	US-09-385-219A-14
4	2270	82.4	443	4	US-09-591-694-8
5	553	20.1	102	4	US-09-621-976-5935
6	194	7.0	39	4	US-09-385-219A-21
7	189	6.9	38	3	US-09-172-841-47
8	189	6.9	38	4	US-08-951-621-47
9	164	6.0	38	3	US-09-172-841-49
10	164	6.0	38	4	US-08-951-621-49
11	144	5.2	321	4	US-09-166-350-15
12	139	5.0	327	4	US-09-591-694-12
13	139	5.0	327	4	US-09-385-219A-58
14	117.5	4.3	503	4	US-09-599-287A-2
15	117	4.2	507	4	US-09-599-287A-24
16	112	4.1	690	4	US-09-248-796A-19169
17	111.5	4.0	506	4	US-09-949-016-11282
18	111.5	4.0	955	4	US-09-949-016-8369
19	110.5	4.0	553	4	US-09-949-016-7961
20	110	4.0	424	4	US-09-538-092-1338
21	109	4.0	3730	4	US-09-949-016-9908
22	107.5	3.9	776	4	US-09-252-991A-28446
23	107	3.9	78	1	US-08-487-359-5
24	107	3.9	78	1	US-08-222-798A-5
25	107	3.9	489	4	US-09-543-681A-7388
26	107	3.9	557	4	US-09-949-016-7621
27	105	3.8	297	4	US-09-252-991A-29217

28	105	3.8	562	4	US-09-949-016-9186	Sequence 9186, Ap
29	104.5	3.8	850	4	US-09-949-016-11324	Sequence 11324, A
30	104	3.8	1312	4	US-09-554-572-26	Sequence 26, Appl
31	103.5	3.8	79	1	US-08-487-359-8	Sequence 8, Appli
32	103.5	3.8	79	1	US-08-222-798A-8	Sequence 8, Appli
33	103.5	3.8	580	3	US-08-906-865-1	Sequence 1, Appli
34	103.5	3.8	580	4	US-09-129-668-1	Sequence 1, Appli
35	103.5	3.8	888	2	US-08-861-464-6	Sequence 6, Appli
36	103.5	3.8	888	2	US-08-396-001-6	Sequence 6, Appli
37	103.5	3.8	888	3	US-09-323-433A-6	Sequence 6, Appli
38	103.5	3.8	888	4	US-09-826-752-6	Sequence 6, Appli
39	103	3.7	133	4	US-09-252-991A-21490	Sequence 21490, A
40	103	3.7	431	4	US-09-248-796A-17260	Sequence 17260, A
41	102.5	3.7	79	1	US-08-487-359-2	Sequence 2, Appli
42	102.5	3.7	79	1	US-08-222-798A-2	Sequence 2, Appli
43	102.5	3.7	644	4	US-09-198-452A-822	Sequence 822, App
44	102.5	3.7	644	4	US-09-438-185A-774	Sequence 774, App
45	102	3.7	141	4	US-09-270-767-38716	Sequence 38716, A

ALIGNMENTS

RESULT 1

US-09-949-016-10867
; Sequence 10867, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10867
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10867

Query Match	99.8%	Score	2748	DB	4	Length	557
Best Local Similarity	99.8%	Pred. NO.	1.5e-255				
Matches	521	Conservative	0	Mismatches	1	Indels	0
Gaps	0						
QY	1	MRLRVLKRTWPLEVPETE	TETGLHLSHRLSLCTWGYSSNTFTITLNYKDPLTGDE	60			
DB	36	MRLRVLKRTWPLEVPETE	PTGLHLSHRLSLCTWGYSSNTFTITLNYKDPLTGDE	95			
QY	61	ETLASYGVSGDLICLI	IQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSSQDEQP	120			
DB	96	ETLASYGVSGDLICLI	IQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSSQDEQP	155			
QY	121	SDSFGQAAQSGVWDD	SMLGPSQNFESIQDNAMAEAGTGTFYPSEPMLCSESVEGQVP	180			
DB	156	SDSFGQAAQSGVWDD	SMLGPSQNFESIQDNAMAEAGTGTFYPSEPMLCSESVEGQVP	215			
QY	181	HSLETLYQSADCS	DANDALIIVLIHLLMESGYIPQGTAKALSMPEKWLKSGVYKLYNH	240			
DB	216	HSLETLYQSADCS	DANDALIIVLIHLLMESGYIPQGTAKALSMPEKWLKSGVYKLYNH	275			
QY	241	PLCEGSSATLTCVPL	GNLIIVNATUKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD	300			
DB	276	PLCEGSSATLTCVPL	GNLIIVNATUKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD	335			
QY	301	LQKLSRLFKDQIVY	PLLAFTFQALNLPDVGVLVPLLELKLRIFFRLDVRSVLSLAVCR	360			

Db 336 LQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLPLELKLRIFRLLDVRSLSAVCR 395
Qy 361 DLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHIORKESPKGRFVMLLPSSSTH 420
Db 396 DLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHIORKESPKGRFVMLLPSSSTH 455
Qy 421 TTFYPNPLHPRFPFSSRLPPGIIGGEYDQRTPLPVVGDPISSLIPGCGTSPQPPPLRP 480
Db 456 TTFYPNPLHPRFPFSSRLPPGIIGGEYDQRTPLPVVGDPISSLIPGCGTSPQPPPLRP 515
Qy 481 REDVPGLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
Db 516 REDVPGLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 557

RESULT 2
US-09-591-694-10
; Sequence 10, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; EARLIER FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US-09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-10

Query Match 99.6%; Score 2744; DB 4; Length 522;
Best Local Similarity 99.6%; Pred. No. 3.2e-255;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLRLKRTWPLEVPEPETEPTLGLHLSRLSLCTWCYSSNTRFTITLNYKDPITGDE 60
Db 1 MRLRVLRLKRTWPLEVPEPETEPTLGLHLSRLSLCTWCYSSNTRFTITLNYKDPITGDE 60
Qy 61 ETLASYGIVSGDLICLILODDIPAPNIPSTDSHSSLQNNQPSLATSSNOTSMQDEQP 120
Db 61 ETLASYGIVSGDLICLILODDIPAPNIPSTDSHSSLQNNQPSLATSSNOTSMQDEQP 120
Qy 121 SDSFQQAQSGVWDDSMGLPSONFEARSIQDNAMHAEGTGYFSEPMLCSESVEGQVP 180
Db 121 SDSFQQAQSGVWDDSMGLPSONFEARSIQDNAMHAEGTGYFSEPMLCSESVEGQVP 180
Qy 181 HSLETLYQSADCSANDALIIVLHLLMLESYIPQTEAKALSMPEKWKLSGVYKLYQYH 240
Db 181 HSLETLYQSADCSANDALIIVLHLLMLESYIPQTEAKALSMPEKWKLSGVYKLYQYH 240
Qy 241 PLCEGSSATLTCVPLGNLIVVWATLKINNEIRSVKRLQLLPSPTCKEKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVVWATLKINNEIRSVKRLQLLPSPTCKEKLGENVANIYKD 300
Qy 301 LQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLPLELKLRIFRLLDVRSLSAVCR 360
Db 301 LQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLPLELKLRIFRLLDVRSLSAVCR 360
Qy 361 DLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHIORKESPKGRFVMLLPSSSTH 420
Db 361 DLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHIORKESPKGRFVMLLPSSSTH 420
Qy 421 TTFYPNPLHPRFPFSSRLPPGIIGGEYDQRTPLPVVGDPISSLIPGCGTSPQPPPLRP 480
Db 421 TTFYPNPLHPRFPFSSRLPPGIIGGEYDQRTPLPVVGDPISSLIPGCGTSPQPPPLRP 480

Qy 481 REDVPGLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
Db 481 REDVPGLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522

RESULT 3
US-09-385-219A-14
; Sequence 14, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiau, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-14

Query Match 90.4%; Score 2489; DB 4; Length 482;
Best Local Similarity 98.1%; Pred. No. 1e-230;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 42 SNRTFTITLNYKDPITGDEETLASYGIVSGDLICLILODDIPAPNIPSTDSHSSLQNN 101
Db 2 SNRTFTITLNYKDPITGDEETLASYGIVSGDLICLILODDIPAPNIPSTDSHSSLQNN 61
Qy 102 BQPSLATSSNOTSMQDEQPSDSFQQAQSGVWDDSMGLPSONFEARSIQDNAMHAEGT 161
Db 62 BQPSLATSSNOTSIQDEQPSDSFQQAQSGVWDDSMGLPSONFEARSIQDNAMHAEGT 121
Qy 162 GFYPSEPMLCSESVEGQVPHSLLETLYQSADCSANDALIIVLHLLMLESYIPQTEAKA 221
Db 122 GFYPSEPMLCSESVEGQVPHSLLETLYQSADCSANDALIIVLHLLMLESYIPQTEAKA 181
Qy 222 LSMPEKWKLSGVYKLYQYMHPLCEGSSATLTCVPLGNLIVVWATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWKLSGVYKLYQYMHPLCEGSSATLTCVPLGNLIVVWATLKINNEIRSVKRLQLLP 241
Qy 282 ESFICEKELGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLPLELKL 341
Db 242 ESFICEKELGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLPLELKL 301
Qy 342 RIFRLLDVRSVLISAVACRDLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHI 401
Db 302 RIFRLLDVRSVLISAVACRDLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFYPNPLHPRFPFSSRLPPGIIGGEYDQRTPLPVGDPI 461
Db 362 QRKESPKGRFVMLLPSSSTHTTIPFYPNPLHPRFPFSSRLPPGIIGGEYDQRTPLPVGDPI 421
Qy 462 SSLIPGCGTSPQPPPLRPFRDTPVGPPLPGRGPNDRPFRPSRGRPTDGRLSF 521
Db 422 SSLIPGCGTSPQPPPLRPFRDTPVGPPLPGRGPNDRPFRPSRGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482

RESULT 4

US-09-591-694-8
; Sequence 8, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-Ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-8

Query Match 82.4%; Score 2270; DB 4; Length 443;
Best Local Similarity 99.8%; Pred. No. 1.1e-209; Mismatches 0; Indels 0; Gaps 0;
Matches 430; Conservative 1;
QY 92 DSEHSLQNNQPSLATSSNOTSMQDEQPSDFQQAQSGVWDDSLMGPSONFEAESI 151
DB 13 DSEHSLQNNQPSLATSSNOTSMQDEQPSDFQQAQSGVWDDSLMGPSONFEAESI 72
QY 152 QNNAHMAECTGYPSEPMCLCSSEVSGQVPHSLTLYQSDADCDANDALIVLHLLMLSSG 211
DB 73 QNNAHMAECTGYPSEPMCLCSSEVSGQVPHSLTLYQSDADCDANDALIVLHLLMLSSG 132
QY 212 YIPOQTEAKALSMPEKWKLVGYKQYHPLCEGSSATLTCVPLGNLIVVNAATLKINNEI 271
DB 133 YIPOQTEAKALSMPEKWKLVGYKQYHPLCEGSSATLTCVPLGNLIVVNAATLKINNEI 192
QY 272 RSVKRLQLLPESFICEKLGENVANIYKDLQKLSRLFKDQVLYPLAFTQALNLPDVF 331
DB 193 RSVKRLQLLPESFICEKLGENVANIYKDLQKLSRLFKDQVLYPLAFTQALNLPDVF 252
QY 332 LVVPLELKLRIFFRLDVRVLSLAVCRDLFTASNDPLLRFLYLRFRDNTVRVQD 391
DB 253 LVVPLELKLRIFFRLDVRVLSLAVCRDLFTASNDPLLRFLYLRFRDNTVRVQD 312
QY 392 WKELYRKHIQKESPKGRFVMLPSSHTTIPFYNPLHPRFPSSRLPPGIIGGEYDOR 451
DB 313 WKELYRKHIQKESPKGRFVMLPSSHTTIPFYNPLHPRFPSSRLPPGIIGGEYDOR 372
QY 452 PTLPVGDPISLIPGGETPQFPPLRPFRFDPVGLPGPNILPGRGPNDRFPFRPSR 511
DB 373 PTLPVGDPISLIPGGETPQFPPLRPFRFDPVGLPGPNILPGRGPNDRFPFRPSR 432
QY 512 GRPTDGRLSFM 522
DB 433 GRPTDGRLSFM 443

RESULT 5

US-09-621-976-5935
; Sequence 5935, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm

; SEQ ID NO 5935

; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 87
; OTHER INFORMATION: Xaa = Cys,Gly
US-09-621-976-5935

Query Match 20.1%; Score 553; DB 4; Length 102;
Best Local Similarity 99.0%; Pred. No. 2.1e-45;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 413 MLLPSSTHTTIPFYNPLHPRFPSSRLPPGIIGGEYDQRTPLPYVGDPISSLIPOGETP 472
DB 1 MLLPSSTHTTIPFYNPLHPRFPSSRLPPGIIGGEYDQRTPLPYVGDPISSLIPOGETP 60
QY 473 SQFPLRFRFDPVGLPGPNILPGRGPNDRFPFRPSR 511
DB 61 SQFPLRFRFDPVGLPGPNILPGRGPNDRFPFRPSR 99

RESULT 6

US-09-385-219A-21
; Sequence 21, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-21

Query Match 7.0%; Score 194; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKLRIFFRLDVRVLSLAVCRDLFTASNDPLLR 373
DB 1 LPLELKLRIFFRLDVRVLSLAVCRDLFTASNDPLLR 39

RESULT 7

US-09-172-841-47
; Sequence 47, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0

```
; SEQ ID NO 47
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-841-47

Query Match
Best Local Similarity 6.9%; Score 189; DB 3; Length 38;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 372
Db 1 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 38

RESULT 8
US-08-951-621-47
; Sequence 47, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-951-621-47

Query Match
Best Local Similarity 6.9%; Score 189; DB 4; Length 38;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 372
Db 1 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 38

RESULT 9
US-09-172-841-49
; Sequence 49, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-172-841-49

Query Match
Best Local Similarity 6.0%; Score 164; DB 3; Length 38;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 372
Db 1 LPLEKLRIFRLLDVRSLSAVCHDLIIASNDPLW 38

RESULT 10
US-08-951-621-49
; Sequence 49, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 49:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-951-621-49

Query Match
Best Local Similarity 6.0%; Score 164; DB 4; Length 38;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 372
Db 1 LPLEKLRIFRLLDVRSLSAVCHDLIIASNDPLW 38

RESULT 11
```

```
US-09-166-350-15
; Sequence 15, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; EARLIER FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-15

Query Match      5.2%; Score 144; DB 4; Length 321;
Best Local Similarity 23.1%; Pred. No. 3.3e-05;
Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;

QY 233 VYKLOYMPLCEG-SATITCVPL-----GNLVNATLKINNE-----TRSV-- 274
Db 35 MPRQWMPFELAGVSSNNLENPCRAAGSLQKTSADTKGQEQAKEKARELFKAVEE 94

QY 275 -----KRLQLLPE-----SFICKEKLGENVANIY-----KDLQKLSRL---FK 309
Db 95 EQNGALYEAKEYRRAMQLVPDIEKITVTRSPDGGVGNVIEDNDDSKWADLLSYFO 154

QY 310 DQLVPLAFTQALNL---PDV-----FGLVPLPLEKLRIFRL-----LDVRSVLSAV 358
Db 155 QQ-----LTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVWSSDLRLSLQSLV 209

QY 359 CRDLTASNDPLRLFLYLRDRDNTVR-VQDTWKELRYKHKIORKESPKGRFVMLLPS 417
Db 210 CRGFICARDPEIWRACLKVGWGRSCKILVPTYSWREMPLE-----PRVFDGVVIS 262

QY 418 ST-----HTIPFPNPLHPRPFSSRLPPGIIGGEYDQRTPLPVGDP 460
Db 263 KTYIRQGEQSLDGFYRAWHQVEY---RYIRFFPDGHV----- 298

QY 461 ISSLIPGGETSPQPPPLRPR 481
Db 299 --MLTTPPEQSIIVRLRTR 317

RESULT 12
US-09-591-694-12
; Sequence 12, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; EARLIER FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 327
; TYPE: PRT

; ORGANISM: Homo sapien
US-09-591-694-12

Query Match      5.0%; Score 139; DB 4; Length 327;
Best Local Similarity 25.1%; Pred. No. 0.0001;
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;

QY 291 GENVANIY-----KDLQKLSRL---FKDQLVPLLAFTQALNL---PDV-----FGLVVLPL 337
Db 19 GDGVGNSYIEDNDDSKWADLLSYFQQ-----LTFQESVLKLCQPELESSQIHISVLP 73

QY 338 ELKLRIFRL-----LDVRSVLSAVCRDLFTASNDPLRLFLYLRDRDNTVR-VQD 391
Db 74 EVLMYIFRWVWSSDLRLSLQSLVCRGFYICARDPEIWRACLKVGWGRSCKILVPTYS 133

QY 392 WKELYRKHKIORKESPKGRFVMLLPSST-----HTIPFPNPLHPRPF 434
Db 134 WREMPLE-----PRVFDGVYISKTYIRQGEQSLDGFYRAWHQVEY---RYIRFF 183

QY 435 PSSRLPPGIIGGEYDQRTPLPVGDPISLSLIPGGETSPQPPPLRPR 481
Db 184 PDGHV-----MLTTPPEQSIIVRLRTR 207

RESULT 13
US-09-385-219A-58
; Sequence 58, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiau, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 58
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-58

Query Match      5.0%; Score 139; DB 4; Length 327;
Best Local Similarity 25.1%; Pred. No. 0.0001;
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;

QY 291 GENVANIY-----KDLQKLSRL---FKDQLVPLLAFTQALNL---PDV-----FGLVVLPL 337
Db 19 GDGVGNSYIEDNDDSKWADLLSYFQQ-----LTFQESVLKLCQPELESSQIHISVLP 73

QY 338 ELKLRIFRL-----LDVRSVLSAVCRDLFTASNDPLRLFLYLRDRDNTVR-VQD 391
Db 74 EVLMYIFRWVWSSDLRLSLQSLVCRGFYICARDPEIWRACLKVGWGRSCKILVPTYS 133

QY 392 WKELYRKHKIORKESPKGRFVMLLPSST-----HTIPFPNPLHPRPF 434
Db 134 WREMPLE-----PRVFDGVYISKTYIRQGEQSLDGFYRAWHQVEY---RYIRFF 183

QY 435 PSSRLPPGIIGGEYDQRTPLPVGDPISLSLIPGGETSPQPPPLRPR 481
Db 184 PDGHV-----MLTTPPEQSIIVRLRTR 207

RESULT 14
US-09-599-287A-2
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